

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 31, 2005, 17:35:30 ; Search time 77 Seconds
(without alignments)
3661.834 Million cell updates/sec

Title: US-10-509-307-1

Perfect score: 4055

Sequence: 1 MAPGTGSSAVNSCPSQLS.....LQPKSQASKPAYGNSPYWTN 786

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues ;

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4055	100.0	786	7 ADP09771	Adp09771 Complete
2	3902	96.2	757	7 ADP09776	Adp09776 JNK3 huma
3	3083	76.0	597	4 AAM93397	Aam93397 Human pol
4	3083	76.0	597	8 ADL30961	Adl30961 Human pro
5	1536	37.9	363	3 RAY9361	Ray9361 Human PRO
6	1536	37.9	363	4 AAB66110	Aab66110 Protein o
7	1536	37.9	363	4 AAU29149	Aau29149 Human PRO
8	1536	37.9	363	6 ABU58525	Abu58525 Human PRO
9	1536	37.9	363	6 ABU88073	Abu88073 Novel hum
10	1536	37.9	363	6 ABU84388	Abu84388 Human sec
11	1536	37.9	363	6 ABR6262	Abr6262 Human sec
12	1536	37.9	363	6 ABR65652	Abr65652 Human sec
13	1536	37.9	363	6 ABU99592	Abu99592 Human sec
14	1536	37.9	363	6 ABU82831	Abu82831 Human PRO
15	1536	37.9	363	6 ABU89952	Abu89952 Novel hum
16	1536	37.9	363	6 ABR68201	Abr68201 Human sec
17	1536	37.9	363	6 ABU98254	Abu98254 Novel hum
18	1536	37.9	363	6 ABU92685	Abu92685 Human sec
19	1536	37.9	363	6 ABO08762	Abu08762 Human sec
20	1536	37.9	363	6 ABO02814	Abu02814 Human sec
21	1536	37.9	363	6 ABR74968	Abr74968 Human sec
22	1536	37.9	363	6 ABR94730	Abr94730 Human sec
23	1536	37.9	363	6 ABR94730	Abu85703 Human PRO
24	1536	37.9	363	6 ABU98863	Abu98863 Novel hum
25	1536	37.9	363	6 ABU98078	Abu98078 Novel hum

26	1536	37.9	363	6 ABU91784	Abu91784 Novel hum
27	1536	37.9	363	6 ABU89477	Abu89477 Human PRO
28	1536	37.9	363	6 ABU86318	Abu86318 Human sec
29	1536	37.9	363	6 ABU67531	Abu67531 Human sec
30	1536	37.9	363	6 ABU80559	Abu80559 Human PRO
31	1536	37.9	363	6 ABR99477	Abr99477 Human sec
32	1536	37.9	363	6 ABR98867	Abr98867 Human sec
33	1536	37.9	363	6 ABO16390	Abu16390 Human sec
34	1536	37.9	363	6 ABR92290	Abr92290 Human sec
35	1536	37.9	363	6 ABO18931	Abu18931 Human sec
36	1536	37.9	363	6 ABR78352	Abr78352 Human sec
37	1536	37.9	363	6 ABU85088	Abu85088 Novel hum
38	1536	37.9	363	6 ABO00227	Abu00227 Novel hum
39	1536	37.9	363	6 ABO11559	Abu11559 Human sec
40	1536	37.9	363	6 ABO02204	Abu02204 Human sec
41	1536	37.9	363	6 ABU88778	Abu88778 Novel hum
42	1536	37.9	363	6 ABU83473	Abu83473 Human sec
43	1536	37.9	363	6 ABO06274	Abu06274 Novel hum
44	1536	37.9	363	6 ABR59310	Abr59310 Human sec
45	1536	37.9	363	6 ABO09372	Abu09372 Human sec

ALIGNMENTS

RESULT 1
ADP09771
ID ADP09771 standard; protein; 786 AA.
XX
AC ADP09771;
XX
DT 29-JUL-2004 (first entry)
XX
DE Complete human KIAA1491 protein sequence.
XX
KW c-Jun phosphorylation; c-Jun N-terminal kinase 3; Nootropic;
KW neuroprotective; Alzheimer's disease; apoptosis; BMAL1; PBPI; KIAA1491;
KW KIAA0596CT; JNK3.
XX
OS Homo sapiens.
XX
FN WO2003086462-A1.
XX
PD 23-OCT-2003.
XX
PF 31-MAR-2003; 2003WO-JP004120.
XX
PR 29-MAR-2002; 2002JP-00095291.
PR 29-MAR-2002; 2002JP-00095390.
PR 29-MAR-2002; 2002JP-00095442.
PR 29-MAR-2002; 2002JP-00095486.
PA (CELE-) CELESTAR LEXICO SCI INC.
PA (DAUC) DAIICHI PHARM CO LTD.
XX
PI Doi H, Wada N, Nakajima H;
XX
XX WPI; 2003-833621/77.
DR N-PSDB; ADP09777.
XX
XX Inhibitors of c-Jun phosphorylation including BMAL1, BPL1, KIAA1491,
PT KIAA0596 and their derivatives, for medical compositions and drugs for
PT treating neurodegenerative diseases e.g. Alzheimer's disease.
XX
XX Claim 1; SEQ ID NO 1; 139pp; Japanese.
PS
XX The present invention relates to inhibitors of c-Jun phosphorylation
XX contain as active ingredient 1 or more peptides that have a function of
CC interacting with c-Jun N-terminal kinase 3. Such peptides can inhibit the
CC phosphorylation or transcription activation of c-Jun, and can also
CC inhibit apoptosis of e.g. nerve cells. Proteins interacting with JNK3
CC were investigated in silico. Then, BMAL1, PBPI, KIAA1491 complete and
CC KIAA0596CT proteins were identified and their interaction with JNK3

CC confirmed. The present sequence represents the complete human KIAA1491
protein sequence.
XX
SQ Sequence 786 AA;
Query Match 100.0%; Score 4055; DB 7; Length 786;
Best Local Similarity 100.0%; Pred. No. 2.2e-236;
Matches 786; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPTGSSSTAVNCSQSSQSSVSLGSGFGLAPPKMANITSSQILDQLKAPSLGQFTTTPS 60
DB 1 MAPTGSSSTAVNCSQSSQSSVSLGSGFGLAPPKMANITSSQILDQLKAPSLGQFTTTPS 60
QY 61 TQONSTSHPTTTSWDLKPTSSQSSVSLSHLDKFSQPEPSVLSQSQSQSQSQAVTVVP 120
DB 61 TQONSTSHPTTTSWDLKPTSSQSSVSLSHLDKFSQPEPSVLSQSQSQSQSQAVTVVP 120
QY 121 PGLSEPPSQAKRESTPGDSPVTKLQLPSTTIENISVHQPQPKHKLAKRIPPA 180
DB 121 PGLSEPPSQAKRESTPGDSPVTKLQLPSTTIENISVHQPQPKHKLAKRIPPA 180
QY 181 SKIPASAVEMPGSADVTGLNVQFGLFEGSEPSLSEFGSAPSENENQIPISLYSKLSE 240
DB 181 SKIPASAVEMPGSADVTGLNVQFGLFEGSEPSLSEFGSAPSENENQIPISLYSKLSE 240
QY 241 PLNTSLMTSAVQNSTYTTTSSVITSCSLTSSSLNASGPMVMSYDQSSVHNRIPIQSPVS 300
DB 241 PLNTSLMTSAVQNSTYTTTSSVITSCSLTSSSLNASGPMVMSYDQSSVHNRIPIQSPVS 300
QY 301 SSESAPGTIMNGHGGRSQQTLDTPKTTGPPSALPSVSLPSTTCTALLPSTSQHTGDL 360
DB 301 SSESAPGTIMNGHGGRSQQTLDTPKTTGPPSALPSVSLPSTTCTALLPSTSQHTGDL 360
QY 361 TSSPLSOLSSSLSHQSSLSHAALSSSTGTHASVESASHQSSATFTFAATSVSSAS 420
DB 361 TSSPLSOLSSSLSHQSSLSHAALSSSTGTHASVESASHQSSATFTFAATSVSSAS 420
QY 421 SGVSLSSMTANSCLCGGTPASASSSSRAAPLVTSGKAPPNLPGQVPLLHNQYLVGP 480
DB 421 SGVSLSSMTANSCLCGGTPASASSSSRAAPLVTSGKAPPNLPGQVPLLHNQYLVGP 480
QY 481 GGLLPAYPIGYDELOMQSLRPVDYIGIPFAAPTALASDRSLANNPYGDTVTKFGRGD 540
DB 481 GGLLPAYPIGYDELOMQSLRPVDYIGIPFAAPTALASDRSLANNPYGDTVTKFGRGD 540
QY 541 SASPAPATTPAQPOQSQSQTHHTAQPPVNPALPGYSYTGLPYTTGMPGAFQVGTMFV 600
DB 541 SASPAPATTPAQPOQSQSQTHHTAQPPVNPALPGYSYTGLPYTTGMPGAFQVGTMFV 600
QY 601 PPASAKQHGVLNSTPTPPFQOASGYGQHYGTGYDDLTQGTAAAGDYSGGYAGSSQAPNK 660
DB 601 PPASAKQHGVLNSTPTPPFQOASGYGQHYGTGYDDLTQGTAAAGDYSGGYAGSSQAPNK 660
QY 661 SAGSGPGKGVSSSTTGLPDMTGSVNKTQTFKQGFHAGTPTPPFSLPSVLGSGTGLAS 720
DB 661 SAGSGPGKGVSSSTTGLPDMTGSVNKTQTFKQGFHAGTPTPPFSLPSVLGSGTGLAS 720
QY 721 GAAPGYAPPFPHLPAHQPHSOLLHHLPODAQSGSGQSQSPSSLOPKQASKPAYGN 780
DB 721 GAAPGYAPPFPHLPAHQPHSOLLHHLPODAQSGSGQSQSPSSLOPKQASKPAYGN 780
QY 781 SPYWTN 786
DB 781 SPYWTN 786
RESULT 2
ADP09776
ID ADP09776 standard; protein; 757 AA.
XX
AC ADP09776;
XX
DT 29-JUL-2004 (first entry)

XX DE
XX KW
XX KW
XX KW
XX KW
XX OS
XX OS
XX FN
XX PD
XX PD
XX PF
XX PR
XX PR
XX PR
XX PR
XX PA
XX PA
XX PI
XX PI
XX DR
XX PT
XX PT
XX PS
XX CC
XX CC
XX CC
XX CC
XX CC
XX CC
XX CC
XX CC
XX SQ
Query Match 96.2%; Score 3902; DB 7; Length 757;
Best Local Similarity 99.9%; Pred. No. 3.6e-227;
Matches 756; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 30 LAPPKMANITSSQILDQLKAPSLGQFTTTPSTQONSTSHPTTTSWDLKPPTSQSSVLSH 89
DB 1 LAPPKMANITSSQILDQLKAPSLGQFTTTPSTQONSTSHPTTTSWDLKPPTSQSSVLSH 60
QY 90 LDFKQPEPSVLSQ 149
DB 61 LDFKQPEPSVLSQ 120
QY 150 LPSTTIENISVHQPQPKHKLAKRIPPAKIPASAVEMPGSADVTGLNVQFGLFEG 209
DB 121 LPSTTIENISVHQPQPKHKLAKRIPPAKIPASAVEMPGSADVTGLNVQFGLFEG 180
QY 210 SEPSLSEFGSAPSENENQIPISLYSKLSEPLNTSLMTSAVQNSTYTTTSSVITSCSLTS 269
DB 181 SEPSLSEFGSAPSENENQIPISLYSKLSEPLNTSLMTSAVQNSTYTTTSSVITSCSLTS 240
QY 270 SSLNASGPMVMSYDQSSVHNRIPIQSPVSSESAPGTIMNGHGGRSQQTLDTPKTTG 329
DB 241 SSLNASGPMVMSYDQSSVHNRIPIQSPVSSESAPGTIMNGHGGRSQQTLDTPKTTG 300
QY 330 PPSALPSVSLPSTTCTALLPSTSQHTGDLTSSPLSOLSSSLSHQSSLSHAALSSST 389
DB 301 PPSALPSVSLPSTTCTALLPSTSQHTGDLTSSPLSOLSSSLSHQSSLSHAALSSST 360

JNK3 human KIAA1491 protein.
c-Jun phosphorylation; c-Jun N-terminal kinase 3; Nootropic;
neuroprotective; Alzheimer's disease; apoptosis; BMAL1; PP1; KIAA1491;
KIAA0596CT; JNK3.
Homo sapiens.
WO2003086462-A1.
23-OCT-2003.
31-MAR-2003; 2003WO-JP004120.
29-MAR-2002; 2002JP-00095291.
29-MAR-2002; 2002JP-00095390.
29-MAR-2002; 2002JP-00095442.
29-MAR-2002; 2002JP-00095486.
(CELE-) CELESTAR LEXICO SCI INC.
(DAUC) DALICHI PHARM CO LTD.
Doi H, Wada N, Nakajima H;
WPI; 2003-833621/77.
Inhibitors of c-Jun phosphorylation including BMAL1, BPL1, KIAA1491,
KIAA0596 and their derivatives, for medical compositions and drugs for
treating neurodegenerative diseases e.g. Alzheimer's disease.

Claim 1; SEQ ID NO 6; 139pp; Japanese.

The present invention relates to inhibitors of c-Jun phosphorylation
contain as active ingredient 1 or more peptides that have a function of
interacting with c-Jun N-terminal kinase 3. Such peptides can inhibit the
phosphorylation or transcription activation of c-Jun, and can also
inhibit apoptosis of e.g. nerve cells. Proteins interacting with JNK3
were investigated in silico. Then, BMAL1, PP1, KIAA1491 complete and
KIAA0596CT proteins were identified and their interaction with JNK3
confirmed. The present sequence represents the complete human JNK3
KIAA1491 protein sequence.

Sequence 757 AA;

QY 390 SHTHASVESASSHOSATFSTAATSVSASSGVSLSMMTANSLCLGGTPASASSSS 449
DB 361 SHTHASVESASSHOSATFSTAATSVSASSGVSLSMMTANSLCLGGTPASASSSS 420
QY 450 RAAPLVTSKAPPNLPQGVPPHLLHNOYLVGPGILLPAYPIYGYDELOQLQSRLPVDYIGI 509
DB 421 RAAPLVTSKAPPNLPQGVPPHLLHNOYLVGPGILLPAYPIYGYDELOQLQSRLPVDYIGI 480
QY 510 PFAAPTALASDRSLANNPYGPDVTKFGRGDSASAPATTTPAQPOQSQSTHTTAQPFV 569
DB 481 PFAAPTALASDRSLANNPYGPDVTKFGRGDSASAPATTTPAQPOQSQSTHTTAQPFV 540
QY 570 NPALPPGVSYTGCLPYTTCMPAFQYGTMTFVPPASAKOHGYNLSTPTPPFQOASGYGQH 629
DB 541 NPALPPGVSYTGCLPYTTCMPAFQYGTMTFVPPASAKOHGYNLSTPTPPFQOASGYGQH 600
QY 630 YSTGYDDLTOGTAAGDYSKGVAGSQAPNKSAGSGPGKGVSVSSTTGLPDMTGSVYNK 689
DB 601 YSTGYDDLTOGTAAGDYSKGVAGSQAPNKSAGSGPGKGVSVSSTTGLPDMTGSVYNK 660
QY 690 TOTFDKQFHAGTTPPPFSLPSVLGSGTGLASGAAPGYAPPPFLHLPAAHQPHSOLLHH 749
DB 661 TOTFDKQFHAGTTPPPFSLPSVLGSGTGLASGAAPGYAPPPFLHLPAAHQPHSOLLHH 720
QY 750 LPQDAQSGSGQRSPSSLOPKSQASKPAYGNSPYWTN 786
DB 721 LPQDAQSGSGQRSPSSLOPKSQASKPAYGNSPYWTN 757

RESULT 3

ID ANM93397 standard; protein; 597 AA.
AC AAM93397;
AC AAM93397;
DT 06-NOV-2001 (first entry)

XX Human polypeptide, SEQ ID NO: 2994.
XX Human; full length cDNA; cDNA synthesis; oligo-capping.
XX Homo sapiens.
XX EPI130094-A2.
XX 05-SEP-2001.
XX 07-JUL-2000; 2000EP-00114089.
XX 08-JUL-1999; 99JP-00194486.
XX 11-JAN-2000; 2000JP-00118774.
XX 02-MAY-2000; 2000JP-00183765.
XX (HELI-) HELIX RES INST.
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2001-524255/58.
XX N-PSDB; AAK94318.

830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.

Claim 8; SEQ ID NO 2994; 1380pp + Sequence Listing; English.

The invention relates to primers for synthesizing full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesizing the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesized by the oligo-capping method. The primers

CC enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
XX Sequence 597 AA;
SQ

Query Match 76.0%; Score 3083; DB 4; Length 597;
Best Local Similarity 99.7%; Pred. No. 8.2e-178;
Matches 595; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 190 MPGADVTGLNVQFALFSGSEPSLSFGSAPSSNSNQIFISLYSKLSPLNTSLMT 249
DB 1 MPGADVTGLNVQFALFSGSEPSLSFGSAPSSNSNQIFISLYSKLSPLNTSLMT 60
QY 250 SAVONSTYTTSVITSCSLTSSLSNSASPVAMSSYDQSSVHNRIPIYQSPVSSSESAPGTI 309
DB 61 SAVONSTYTTSVITSCSLTSSLSNSASPVAMSSYDQSSVHNRIPIYQSPVSSSESAPGTI 120
QY 310 MNGHGGGRSQOTLDTPTKTGPPSALPSVSSLPSTTCTALLPSTSOHTGDLTSSPLSOLS 369
DB 121 MNGHGGGRSQOTLDTPTKTGPPSALPSVSSLPSTTCTALLPSTSOHTGDLTSSPLSOLS 180
QY 370 SSLSSHQSSLSAHAALSSSTSHTHASVESASSHQSSTATFTAAATSVSSASSGVSLSSSM 429
DB 181 SSLSSHQSSLSAHAALSSSTSHTHASVESASSHQSSTATFTAAATSVSSASSGVSLSSSM 240
QY 430 NTANSLCIGGTPASASSSSRAAPLVTSGKAPPNLPGVPPHLLHNOYLVGPGILLPAYPI 489
DB 241 NTANSLCIGGTPASASSSSRAAPLVTSGKAPPNLPGVPPHLLHNOYLVGPGILLPAYPI 300
QY 490 YGYDELOQLQSRLPVDYIGIPFAAPTALASDRSLANNPYGPDVTKFGRGDSASAPATT 549
DB 301 YGYDELOQLQSRLPVDYIGIPFAAPTALASDRSLANNPYGPDVTKFGRGDSASAPATT 360
QY 550 PAQPOQSOSQTHHTTAQPFVNPALPGYSYTGTPFYTGMPSAFOYGTMTFVPPASAKOHG 609
DB 361 PAQPOQSOSQTHHTTAQPFVNPALPGYSYTGTPFYTGMPSAFOYGTMTFVPPASAKOHG 420
QY 610 VNLSTPTPPFQOASGYGQHGYSYGYDDLTQGTAAAGDYSKGVAGSQAPNKSAGSGPGKG 669
DB 421 VNLSTPTPPFQOASGYGQHGYSYGYDDLTQGTAAAGDYSKGVAGSQAPNKSAGSGPGKG 480
QY 670 VSVSSSTTGLPDMTGSVYNKTFQFDKQFHAGTTPPPFSLPSVLGSGTGLASGAAPGYAPP 729
DB 481 VSVSSSTTGLPDMTGSVYNKTFQFDKQFHAGTTPPPFSLPSVLGSGTGLASGAAPGYAPP 540
QY 730 PFLHILPAHQPHSOLLHLLPQDAQSGSGQRSPSSLOPKSQASKPAYGNSPYWTN 786
DB 541 PFLHILPAHQPHSOLLHLLPQDAQSGSGQRSPSSLOPKSQASKPAYGNSPYWTN 597

RESULT 4

ADL30961
ID ADL30961 standard; protein; 597 AA.
AC ADL30961;
AC ADL30961;
DT 20-MAY-2004 (first entry)

Human protein encoded by a full length cDNA clone SeqID 2994.

human; medicine; signal transduction; glycoprotein; transcription; oligo-capping method.

Homo sapiens.

OS OS

XX EPI1396543-A2.

XX PN

XX PD 10-MAR-2004.

XX PF 07-JUL-2000; 2003EP-00025638.

XX 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183865.
PR 07-JUL-2000; 2000JP-00114089.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Ota T, Nishikawa T, Isogai T, Hayaashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2004-204755/20.
DR N-PSDB; ADL30960.
XX New oligonucleotide primers (830 cDNAs) useful for synthesizing full
PT length human cDNAs.
XX Example 1; SEQ ID NO 2994; 1340pp; English.
XX This invention relates to a novel primers useful for synthesizing full
CC length cDNA molecules that encode human proteins. Specifically, it refers
CC to secretory or membrane proteins that are potential therapeutic agents/
CC target molecules in the field of medicine, and in particular genes
CC encoding proteins that are associated with signal transduction.
CC glycoproteins and transcription. The present invention describes a method
CC for efficiently cloning a full length human cDNA from both the 5' and 3'
CC ends using the oligo-capping method. This polypeptide sequence is a full
CC length human protein of the invention.
XX SQ Sequence 597 AA;
Query Match 76.0%; Score 3083; DB 8; Length 597;
Best Local Similarity 99.7%; Pred. No. 8.2e-178;
Matches 595; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 190 MFGADVTGLNVQGALEFGEPSLSEFGAPSENENQIPISLYSKSLSEPLNTLSMT 249
DB 1 MFGADVTGLNVQGALEFGEPSLSEFGAPSENENQIPISLYSKSLSEPLNTLSMT 60
QY 250 SAVQNSTYTTTSVITSCSLTSSLSNASFVAMSSSYDQSSVHNRIPIQSPVSSSESAPGTI 309
DB 61 SAVQNSTYTTTSVITSCSLTSSLSNASFVAMSSSYDQSSVHNRIPIQSPVSSSESAPGTI 120
QY 310 MNGHGGGRSQOTLTPKTTGPPSALPVSSLSPTSTCTALLPSTSOHTGDLTSSPLSOLS 369
DB 121 MNGHGGGRSQOTLTPKTTGPPSALPVSSLSPTSTCTALLPSTSOHTGDLTSSPLSOLS 180
QY 370 SSLSHQSSLSAHAALSSSTSHASVESASHQSSATFTTAATSVSSASSGVSLSSSM 429
DB 181 SSLSHQSSLSAHAALSSSTSHASVESASHQSSATFTTAATSVSSASSGVSLSSSM 240
QY 430 NTANSLCLGGTPASASSSSRAAPLVTSGKAPPNLPQGVPPLLINQVLVPGGLLPAYPI 489
DB 241 NTANSLCLGGTPASASSSSRAAPLVTSGKAPPNLPQGVPPLLINQVLVPGGLLPAYPI 300
QY 490 YGYDELOMLQSLPVDYVYIGIFPAAPTALASRDRLANNPYDGVTKFGRGDSASAPATT 549
DB 301 YGYDELOMLQSLPVDYVYIGIFPAAPTALASRDRLANNPYDGVTKFGRGDSASAPATT 360
QY 550 PAQPOQSOQTHHTAQOQFVNPALPPGYSTGLPYTGMPSAFQYGTMTFVPPASAKQHG 609
DB 361 PAQPOQSOQTHHTAQOQFVNPALPPGYSTGLPYTGMPSAFQYGTMTFVPPASAKQHG 420
QY 610 VNLSTPTPPFOAQSGYGHGTYGVDLTOGTAAQDYKGGYAGSSQAPNKSAGSGPKG 669
DB 421 VNLSTPTPPFOAQSGYGHGTYGVDLTOGTAAQDYKGGYAGSSQAPNKSAGSGPKG 480
QY 670 VSVSSSTTGLPMTGSGVYKNTQTFKQGFHAGTTPPFSPLPSVLGSGTGLASGAAPGYAPP 729
DB 481 VSVSSSTTGLPMTGSGVYKNTQTFKQGFHAGTTPPFSPLPSVLGSGTGLASGAAPGYAPP 540
QY 730 PFLHILPAHQPHSQSLHLLHLLPQDAQSGSQRSQPSLQPKSQASKPAYGNSPYWTN 786

Db 541 PFLHILPAHQPHSQSLHLLHLLPQDAQSGSQRSQPSLQPKSQASKPAYGNSPYWTN 597
RESULT 5
AAY99361
ID AAY99361 standard; protein; 363 AA.
XX AAY99361;
AC AAY99361;
XX 08-AUG-2000 (first entry)
XX Human PRO1197 (UNQ610) amino acid sequence SEQ ID NO:72.
XX Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
KW transmembrane; secretion; immunoadhesion; pharmaceutical; screening.
XX Homo sapiens.
XX WO200012708-A2.
XX 09-MAR-2000.
PF 01-SEP-1999; 99WO-US020111.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098749P.
PR 01-SEP-1998; 98US-0098750P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
PR 02-SEP-1998; 98US-00989536P.
PR 09-SEP-1998; 98US-0099596P.
PR 09-SEP-1998; 98US-0099598P.
PR 09-SEP-1998; 98US-0099602P.
PR 09-SEP-1998; 98US-0099642P.
PR 09-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099792P.
PR 10-SEP-1998; 98US-0099808P.
PR 10-SEP-1998; 98US-0099812P.
PR 10-SEP-1998; 98US-0099815P.
PR 10-SEP-1998; 98US-0099818P.
PR 15-SEP-1998; 98US-0100383P.
PR 15-SEP-1998; 98US-0100388P.
PR 15-SEP-1998; 98US-0100390P.
PR 16-SEP-1998; 98US-0100584P.
PR 16-SEP-1998; 98US-0100627P.
PR 16-SEP-1998; 98US-0100661P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100710P.
PR 17-SEP-1998; 98US-0100711P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100848P.
PR 18-SEP-1998; 98US-0100849P.
PR 18-SEP-1998; 98US-0101014P.
PR 18-SEP-1998; 98US-0101068P.
PR 18-SEP-1998; 98US-0101071P.
PR 22-SEP-1998; 98US-0101279P.
PR 23-SEP-1998; 98US-0101471P.
PR 23-SEP-1998; 98US-0101472P.
PR 23-SEP-1998; 98US-0101474P.
PR 23-SEP-1998; 98US-0101475P.
PR 23-SEP-1998; 98US-0101476P.
PR 23-SEP-1998; 98US-0101477P.
PR 23-SEP-1998; 98US-0101479P.
PR 23-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101741P.
PR 24-SEP-1998; 98US-0101743P.

PF	18-FEB-2000; 2000WO-US004342.	DT	18-DEC-2001 (first entry)
XX		XX	Human PRO polypeptide sequence #126.
PR	23-JUN-1999; 99US-0141037P.	DE	
PR	20-JUL-1999; 99US-0144758P.	XX	PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
PR	26-JUL-1999; 99US-0145698P.	KW	dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
PR	01-SEP-1999; 99WO-US020111.	KW	blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
PR	29-OCT-1999; 99US-0162506P.	KW	adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
PR	30-NOV-1999; 99WO-US028313.	XX	
PR	02-DEC-1999; 99WO-US028551.	OS	Homo sapiens.
PR	16-DEC-1999; 99WO-US030095.	XX	
PR	05-JAN-2000; 2000WO-US000219.	PN	WO200168848-A2.
PR	06-JAN-2000; 2000WO-US000376.	XX	
XX		XX	20-SEP-2001.
PA	(GETH) GENENTECH INC.	PD	
XX		XX	28-FEB-2001; 2001WO-US006520.
PI	Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;	PF	
PI	Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;	XX	01-MAR-2000; 2000WO-US005601.
PI	Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;	PR	02-MAR-2000; 2000WO-US005841.
PI	Williams PM, Wood WI;	PR	03-MAR-2000; 2000US-0187202P.
XX		PR	06-MAR-2000; 2000US-0186968P.
XX	WPI; 2001-071395/08.	PR	14-MAR-2000; 2000US-0189320P.
DR		PR	14-MAR-2000; 2000US-0189328P.
XX		PR	15-MAR-2000; 2000WO-US006884.
XX	Secreted and transmembrane proteins and nucleic acids designated PRO,	PR	21-MAR-2000; 2000US-0190828P.
PT	useful as hybridization probes, in chromosome and gene mapping and gene	PR	21-MAR-2000; 2000US-0191007P.
PT	therapy.	PR	21-MAR-2000; 2000US-0191048P.
XX		PR	21-MAR-2000; 2000US-0191314P.
PS	Claim 1; Fig 44; 787pp; English.	PR	21-MAR-2000; 2000US-0192655P.
XX		PR	28-MAR-2000; 2000US-0193032P.
CC	The present invention relates to secreted and transmembrane proteins.	PR	29-MAR-2000; 2000US-0193053P.
CC	These proteins and the DNA encoding them may be used as hybridization	PR	29-MAR-2000; 2000WO-US008439.
CC	probes, in chromosome and gene mapping and in the generation of anti-	PR	30-MAR-2000; 2000WO-US008439.
CC	sense RNA and DNA. They may also be used to generate either	PR	04-APR-2000; 2000US-0194449P.
CC	transgenic animals or knockout animals which are in turn useful for	PR	04-APR-2000; 2000US-0194647P.
CC	development and screening of therapeutically useful reagents. The nucleic	PR	11-APR-2000; 2000US-0195975P.
CC	acids may also be used in gene therapy	PR	11-APR-2000; 2000US-0196000P.
XX		PR	11-APR-2000; 2000US-0196187P.
XX	Sequence 363 AA;	PR	11-APR-2000; 2000US-0196690P.
QY	Query Match 37.9%; Score 1536; DB 4; Length 363;	PR	11-APR-2000; 2000US-0196820P.
Db	Best Local Similarity 96.2%; Pred. No. 1.3e-84;	PR	18-APR-2000; 2000US-0198121P.
	Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;	PR	18-APR-2000; 2000US-0198585P.
QY	7 SSTAIVSCS--PQSLSSVLGSGFGLAPPKXANITSSQILDQLKAPSLGQFTTTPSTQON 64	PR	25-APR-2000; 2000US-0199397P.
Db	9 NSVLIRICSFPLLLKSSVLGSGFGLAPPKXANITSSQILDQLKAPSLGQFTTTPSTQON 68	PR	25-APR-2000; 2000US-0199550P.
QY	65 STSHPTTTTMDLKPTTSQSSVLSHLDPKSQPEPSPVLSQLSQHQHQSQAATVPPPGLE 124	PR	25-APR-2000; 2000US-0199654P.
Db	69 STSHPTTTTMDLKPTTSQSSVLSHLDPKSQPEPSPVLSQLSQHQHQSQAATVPPPGLE 128	PR	03-MAY-2000; 2000US-0201516P.
QY	125 SPFSQAKLRESTPGDSPSTVKNLLQLPSTTIENISVSHQPPQPKHKLAKRIPPASKIP 184	PR	17-MAY-2000; 2000WO-US013705.
Db	129 SPFSQAKLRESTPGDSPSTVKNLLQLPSTTIENISVSHQPPQPKHKLAKRIPPASKIP 188	PR	22-MAY-2000; 2000WO-US014042.
QY	185 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFEGSAPSENSNQIPISLXSKLSLEPLNT 244	PR	30-MAY-2000; 2000WO-US015264.
Db	189 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFEGSAPSENSNQIPISLXSKLSLEPLNT 248	PR	02-JUN-2000; 2000US-0209832P.
QY	245 SLSMTSAVQNSTYTSVTITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304	PR	28-JUL-2000; 2000WO-US020710.
Db	249 SLSMTSAVQNSTYTSVTITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308	PR	22-AUG-2000; 2000US-00644848.
QY	305 APGTIMNGHGGRSQOTLDT 324	PR	24-AUG-2000; 2000WO-US023328.
Db	309 APGTIMNGHGGRSQOTLDS 328	PR	08-NOV-2000; 2000WO-US030952.
		PR	01-DEC-2000; 2000WO-US032678.
		PR	20-DEC-2000; 2000WO-US034956.
RESULT 7		XX	(GETH) GENENTECH INC.
AAU29149		XX	Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
ID AAU29149 standard; protein; 363 AA.		PI	Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX		XX	WPI; 2001-602746/68.
AC		DR	N-PSDB; AAS46050.
XX		DR	Novel nucleic acids encoding PRO polypeptides, used to diagnose the
		PT	presence of tumors, such as prostate and breast tumors, in mammals and to
		PT	screen for modulators of the compounds.
		XX	Claim 11; Fig 252; 774pp; English.
		PS	Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
		CC	The PRO polypeptides and their associated nucleic acids can be used to
XX		CC	

RESULT 8	
ABU58525	
ID	ABU58525 standard; protein; 363 AA.
XX	
AC	ABU58525;
XX	
DT	15-APR-2003 (first entry)
XX	
DE	Human PRO polypeptide #126.
XX	
KW	Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW	dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW	antibody-dependent enzyme mediated prodrug therapy.
XX	
OS	Homo sapiens.
XX	
PN	US2003027272-A1.
XX	
PD	06-FEB-2003.
XX	
PF	21-JUN-2002; 2002US-00176492.
XX	
PR	18-SEP-1997; 97US-0059263P.
PR	18-SEP-1997; 97US-0059266P.
PR	17-OCT-1997; 97US-0062250P.
PR	21-OCT-1997; 97US-0063486P.
PR	24-OCT-1997; 97US-0063120P.

PR	10-JUN-1998;	98US-0088826P.
PR	11-JUN-1998;	98US-0088861P.
PR	11-JUN-1998;	98US-0088863P.
PR	11-JUN-1998;	98US-0088876P.
PR	12-JUN-1998;	98US-0089090P.
PR	12-JUN-1998;	98US-0089105P.
PR	13-JUN-1998;	98US-0089512P.
PR	16-JUN-1998;	98US-0089514P.
PR	17-JUN-1998;	98US-0089388P.
PR	17-JUN-1998;	98US-0089598P.
PR	17-JUN-1998;	98US-0089653P.
PR	18-JUN-1998;	98US-0089908P.
PR	19-JUN-1998;	98US-0089952P.
PR	22-JUN-1998;	98US-0090252P.
PR	22-JUN-1998;	98US-0090254P.
PR	22-JUN-1998;	98US-0090429P.
PR	24-JUN-1998;	98US-0090435P.
PR	24-JUN-1998;	98US-0090441P.
PR	24-JUN-1998;	98US-0090535P.
PR	24-JUN-1998;	98US-0090540P.
PR	24-JUN-1998;	98US-0090676P.
PR	25-JUN-1998;	98US-0090678P.
PR	25-JUN-1998;	98US-0090688P.
PR	25-JUN-1998;	98US-0090690P.
PR	25-JUN-1998;	98US-0090694P.
PR	25-JUN-1998;	98US-0090695P.
PR	25-JUN-1998;	98US-0090696P.
PR	26-JUN-1998;	98US-00105413.
PR	26-JUN-1998;	98US-0090862P.
PR	26-JUN-1998;	98US-0090863P.
PR	26-JUN-1998;	98US-0091010P.
PR	01-JUL-1998;	98US-0091359P.
PR	01-JUL-1998;	98US-0091544P.
PR	02-JUL-1998;	98US-0091478P.
PR	02-JUL-1998;	98US-0091486P.
PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091632P.
PR	24-JUL-1998;	98US-0094006P.
PR	04-AUG-1998;	98US-0095282P.
PR	10-AUG-1998;	98US-0095998P.
PR	10-AUG-1998;	98US-0096012P.
PR	17-AUG-1998;	98US-0096757P.
PR	17-AUG-1998;	98US-0096867P.
PR	17-AUG-1998;	98US-0096891P.
PR	17-AUG-1998;	98US-0096897P.
PR	18-AUG-1998;	98US-0096949P.
PR	18-AUG-1998;	98US-0096959P.
PR	18-AUG-1998;	98US-0097022P.
PR	26-AUG-1998;	98US-0097952P.
PR	26-AUG-1998;	98US-0097954P.
PR	26-AUG-1998;	98US-0097955P.
PR	26-AUG-1998;	98US-0097971P.
PR	26-AUG-1998;	98US-0097974P.
PR	26-AUG-1998;	98US-0098014P.
PR	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098723P.
PR	02-SEP-1998;	98US-0098803P.
PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
PR	09-SEP-1998;	98US-0099602P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099812P.
PR	13-SEP-1998;	98US-0100388P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	16-SEP-1998;	98US-0101751P.
PR	16-SEP-1998;	98WO-US019330.
PR	17-SEP-1998;	98US-0100683P.
PR	17-SEP-1998;	98US-0100684P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101477P.
PR	24-SEP-1998;	98US-0101738P.
PR	24-SEP-1998;	98US-0101739P.
PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101922P.
PR	25-SEP-1998;	98US-0101786P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
PR	06-OCT-1998;	98US-0103449P.
PR	07-OCT-1998;	98US-00168978.
PR	07-OCT-1998;	98US-00168978.
Query Match 37.9%; Score 1536; DB 6; Length 363;		
Best Local Similarity 96.2%; Pred. No. 1.3e-84; Indels 2; Gaps 1;		
Matches 308; Conservative 3; Mismatches 7;		
QY	7	SSTAVNSCS--PQSLSVLGSGFGLAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON 64
DB	9	NSVLIRICSFIPLLKSSVLGSGFGLAPPKMANITSSQILDQLKAPSLGQFTTTPSTQON 68
QY	65	STSHPTTTTSDWKPTTSQSSVLGSHLDPKSPVLSQSQHQHQSOAVTTPPGCLE 124
DB	69	STSHPTTTTSDWKPTTSQSSVLGSHLDPKSPVLSQSQHQHQSOAVTTPPGCLE 128
QY	125	SFPSQAKLRESTPGDSPSTVKNLLQLPSTTIENISVSVHQPKHIKAKRIRIPASKIP 184
DB	129	SFPSQAKLRESTPGDSPSTVKNLLQLPSTTIENISVSVHQPKHIKAKRIRIPASKIP 188
QY	185	ASAVEMPGSADVTGLNVQFGLFSGSEPSLSEFGSAPSSSENSNQIPISLYSKLSLEPLNT 244
DB	189	ASAVEMPGSADVTGLNVQFGLFSGSEPSLSEFGSAPSSSENSNQIPISLYSKLSLEPLNT 248
QY	245	SLSMTSAVQNSVTYTSVITSCSLTSSSLNSASPVAMSSSYDOSSVHNRIPIQSPVSSSES 304
DB	249	SLSMTSAVQNSVTYTSVITSCSLTSSSLNSASPVAMSSSYDOSSVHNRIPIQSPVSSSES 308
QY	305	APGTINMGHGGGRSQOTLDT 324
DB	309	APGTINMGHGGGRSQOTLDS 328
RESULT 9		
ABU88073		
ID	ABU88073 standard; protein; 363 AA.	
XX	AC	
XX	ABU88073;	
XX	07-JUL-2003 (first entry)	
XX	Novel human secreted and transmembrane protein PRO1197.	
DE	Human; secreted and transmembrane protein; PRO; gene therapy;	
XX	tumour necrosis factor-alpha release; TNF-alpha release;	
KW	chondrocyte proliferation; chondrocyte differentiation; tumour;	
KW	adrenal tumour; lung tumour; colon tumour; breast tumour;	

KW prostate tumour; rectal tumour; cervical tumour; liver tumour.

OS Homo sapiens.

XX US2003032127-A1.

PN 13-FEB-2003.

XX 26-JUN-2002; 2002US-00183012.

XX 18-SEP-1997; 97US-0059263P.

PR 18-SEP-1997; 97US-0059266P.

PR 17-OCT-1997; 97US-0082250P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 28-OCT-1997; 97US-0063540P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063734P.

PR 31-OCT-1997; 97US-0063870P.

PR 31-OCT-1997; 97US-0064103P.

PR 13-NOV-1997; 97US-0065311P.

PR 21-NOV-1997; 97US-0066120P.

PR 24-NOV-1997; 97US-0066466P.

PR 24-NOV-1997; 97US-0066772P.

PR 11-DEC-1997; 97US-0069335P.

PR 12-DEC-1997; 97US-0069425P.

PR 17-DEC-1997; 97US-0069870P.

PR 18-DEC-1997; 97US-0068017P.

PR 10-MAR-1998; 98US-0077450P.

PR 11-MAR-1998; 98US-0077632P.

PR 11-MAR-1998; 98US-0077649P.

PR 20-MAR-1998; 98US-0078886P.

PR 20-MAR-1998; 98US-0078939P.

PR 27-MAR-1998; 98US-0079664P.

PR 27-MAR-1998; 98US-0079786P.

PR 31-MAR-1998; 98US-0080107P.

PR 31-MAR-1998; 98US-0080194P.

PR 01-APR-1998; 98US-0080327P.

PR 01-APR-1998; 98US-0080333P.

PR 08-APR-1998; 98US-0081049P.

PR 08-APR-1998; 98US-0081070P.

PR 09-APR-1998; 98US-0081195P.

PR 04-JUN-1998; 98US-0088028P.

PR 04-JUN-1998; 98US-0088029P.

PR 04-JUN-1998; 98US-0088033P.

PR 05-JUN-1998; 98US-0088326P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088202P.

PR 05-JUN-1998; 98US-0088212P.

PR 05-JUN-1998; 98US-0088217P.

PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088722P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088740P.

PR 10-JUN-1998; 98US-0088811P.

PR 10-JUN-1998; 98US-0088824P.

PR 10-JUN-1998; 98US-0088825P.

PR 10-JUN-1998; 98US-0088826P.

PR 11-JUN-1998; 98US-0088861P.

PR 11-JUN-1998; 98US-0088863P.

PR 11-JUN-1998; 98US-0088876P.

PR 12-JUN-1998; 98US-0089090P.

PR 12-JUN-1998; 98US-0089105P.

PR 16-JUN-1998; 98US-0089512P.

PR 16-JUN-1998; 98US-0089514P.

PR 17-JUN-1998; 98US-0089538P.

PR 17-JUN-1998; 98US-0089598P.

PR 17-JUN-1998; 98US-0089653P.

PR 18-JUN-1998; 98US-0089908P.

PR 19-JUN-1998; 98US-0089952P.

PR 22-JUN-1998; 98US-0090246P.

PR 22-JUN-1998; 98US-0090252P.

PR 22-JUN-1998; 98US-0090254P.

PR 24-JUN-1998; 98US-0090429P.

PR 24-JUN-1998; 98US-0090435P.

PR 24-JUN-1998; 98US-0090444P.

PR 24-JUN-1998; 98US-0090461P.

PR 24-JUN-1998; 98US-0090535P.

PR 24-JUN-1998; 98US-0090540P.

PR 25-JUN-1998; 98US-0090676P.

PR 25-JUN-1998; 98US-0090678P.

PR 25-JUN-1998; 98US-0090688P.

PR 25-JUN-1998; 98US-0090690P.

PR 25-JUN-1998; 98US-0090694P.

PR 25-JUN-1998; 98US-0090695P.

PR 25-JUN-1998; 98US-0090696P.

PR 26-JUN-1998; 98US-00105413.

PR 26-JUN-1998; 98US-0090862P.

PR 26-JUN-1998; 98US-0090863P.

PR 26-JUN-1998; 98US-0091010P.

PR 01-JUL-1998; 98US-0091359P.

PR 02-JUL-1998; 98US-0091544P.

PR 02-JUL-1998; 98US-0091478P.

PR 02-JUL-1998; 98US-0091486P.

PR 02-JUL-1998; 98US-0091626P.

PR 02-JUL-1998; 98US-0091628P.

PR 02-JUL-1998; 98US-0091632P.

PR 04-AUG-1998; 98US-0094006P.

PR 10-AUG-1998; 98US-0095282P.

PR 10-AUG-1998; 98US-0095988P.

PR 10-AUG-1998; 98US-0096012P.

PR 17-AUG-1998; 98US-0096757P.

PR 17-AUG-1998; 98US-0096766P.

PR 17-AUG-1998; 98US-0096867P.

PR 17-AUG-1998; 98US-0096891P.

PR 17-AUG-1998; 98US-0096897P.

PR 18-AUG-1998; 98US-0096949P.

PR 18-AUG-1998; 98US-0096959P.

PR 18-AUG-1998; 98US-0097022P.

PR 26-AUG-1998; 98US-0097952P.

PR 26-AUG-1998; 98US-0097954P.

PR 26-AUG-1998; 98US-0097955P.

PR 26-AUG-1998; 98US-0097971P.

PR 26-AUG-1998; 98US-0097974P.

PR 26-AUG-1998; 98US-0098014P.

PR	01-SEP-1998;	98US-0098716P.	ABU84388	
PR	02-SEP-1998;	98US-0098723P.	ID	ABU84388 standard; protein; 363 AA.
PR	02-SEP-1998;	98US-0098803P.	XX	
PR	02-SEP-1998;	98US-0098821P.	AC	ABU84388;
PR	02-SEP-1998;	98US-0098843P.	XX	
PR	09-SEP-1998;	98US-0099602P.	DT	02-AUG-2003 (first entry)
PR	10-SEP-1998;	98US-0099741P.	XX	
PR	10-SEP-1998;	98US-0099754P.	XX	Human secreted/transmembrane protein (PRO) #126.
PR	10-SEP-1998;	98US-0099763P.	DE	
PR	10-SEP-1998;	98US-0099812P.	XX	Human; secreted and transmembrane protein; PRO; TNF-alpha;
PR	15-SEP-1998;	98US-0100388P.	KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
PR	16-SEP-1998;	98US-0100662P.	KW	tissue typing.
PR	16-SEP-1998;	98US-0100664P.	XX	
PR	16-SEP-1998;	98US-0101751P.	XX	
PR	16-SEP-1998;	98US-0101933P.	OS	Homo sapiens.
PR	17-SEP-1998;	98US-0100683P.	XX	
PR	17-SEP-1998;	98US-0100684P.	XX	
PR	17-SEP-1998;	98US-0100919P.	PN	US2003032112-A1.
PR	17-SEP-1998;	98US-0100930P.	XX	
PR	18-SEP-1998;	98US-0100849P.	XX	13-FEB-2003.
PR	18-SEP-1998;	98US-0101014P.	XX	
PR	18-SEP-1998;	98US-0101068P.	XX	
PR	23-SEP-1998;	98US-0101471P.	XX	21-JUN-2002; 2002US-00176756.
PR	23-SEP-1998;	98US-0101472P.	XX	
PR	23-SEP-1998;	98US-0101475P.	PR	18-SEP-1997; 97US-0059263P.
PR	23-SEP-1998;	98US-0101477P.	PR	18-SEP-1997; 97US-0059266P.
PR	24-SEP-1998;	98US-0101738P.	PR	17-OCT-1997; 97US-0062250P.
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KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	289.5	7.1	1306	US-09-538-092-330	Sequence 330, App
4	289	7.1	336	US-09-270-767-43343	Sequence 43343, A
5	287.5	7.1	2870	US-09-479-467A-15	Sequence 15, Appl
6	287.5	7.1	3178	US-09-479-467A-4	Sequence 4, Appl
7	286.5	7.1	2090	US-09-538-092-1081	Sequence 1081, Ap
8	282.5	7.0	2137	US-09-134-001C-4463	Sequence 4463, Ap
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11	269	6.6	827	US-09-248-796A-17307	Sequence 17307, A
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13	260.5	6.4	2032	US-09-854-856-42	Sequence 42, Appl
14	260.5	6.4	2062	US-09-854-856-26	Sequence 26, Appl
15	260.5	6.4	2094	US-09-854-856-10	Sequence 10, Appl
16	260.5	6.4	2141	US-09-854-856-56	Sequence 56, Appl
17	260.5	6.4	2157	US-09-854-856-52	Sequence 52, Appl
18	260.5	6.4	2169	US-09-854-856-40	Sequence 40, Appl
19	260.5	6.4	2185	US-09-854-856-36	Sequence 36, Appl
20	260.5	6.4	2201	US-09-854-856-24	Sequence 24, Appl
21	260.5	6.4	2217	US-09-854-856-20	Sequence 20, Appl
22	260.5	6.4	2229	US-09-854-856-8	Sequence 8, Appl
23	260.5	6.4	2245	US-09-854-856-4	Sequence 4, Appl
24	260.5	6.4	2294	US-09-854-856-50	Sequence 50, Appl
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32	258.5	6.4	2048	4	US-09-854-856-62	Sequence 62, Appl
33	258.5	6.4	2076	4	US-09-854-856-46	Sequence 46, Appl
34	258.5	6.4	2108	4	US-09-854-856-30	Sequence 30, Appl
35	258.5	6.4	2136	4	US-09-854-856-14	Sequence 14, Appl
36	249.5	6.2	610	4	US-09-538-092-1378	Sequence 1378, Ap
37	249	6.1	1142	2	US-08-993-118-7	Sequence 7, Appl
38	249	6.1	1142	3	US-08-845-528C-7	Sequence 7, Appl
39	249	6.1	1142	4	US-09-066-281B-7	Sequence 7, Appl
40	249	6.1	1142	4	US-09-468-433C-7	Sequence 7, Appl
41	248.5	6.1	1093	3	US-08-545-860D-55	Sequence 55, Appl
42	248.5	6.1	1093	5	PCT-US94-04496-55	Sequence 55, Appl
43	246	6.1	1142	3	US-09-061-709-2	Sequence 2, Appl
44	246	6.1	1142	4	US-09-899-651-2	Sequence 2, Appl
45	246	6.1	1142	4	US-09-392-714-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-09-538-092-1320
; Sequence 1320, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 1320
; LENGTH: 983
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14157
US-09-538-092-1320

Query Match						30.8%; Score 1248.5; DB 4; Length 983;
Best Local Similarity						45.1%; Pred. No. 3.9e-76;
Matches						307; Conservative 98; Mismatches 188; Indels 87; Gaps 27;
Qy	3	PGTGSSTAVNSCPQSLSVLSGSGFGLAPPKMANITSSQILDQLK-APSLGQFTTTPST	61			
Db	327	PASG-----NTFSHSHSVMSLKGFGDVGAKGSGTTGSGFLEQFKTAQALAA----	377			
Qy	62	QQNSTSHPTTTTNDLKPPTSQSVLSHLDFKQPEPSPVLSQLSQRQ-----	109			
Db	378	-QHSQSGSTTTSSWDM-GSTTQPSLVQYDLKN-PSDSAVHSPFTKRAQTPSSTMMEVF	434			
Qy	110	-QHSQAV----TVPPGLESFPQAKLRSTGDSFTVKNKLIQLESTTIENTISVSHQ	164			
Db	435	LOEKSPAVATSTAAPPSPSPPLPSKS---TSAPQSPGSDNQSSP-----	479			
Qy	165	POPKHKLAKRTPPASKIPASAVEMPGSDVTLNVQFGLGEPSPSLSEFGSAP--SS	223			
Db	480	PAQQLKQKKKASLTSKIPALAVEMPGSADISGLNQFGLQFSGEPVLSDYESTPTS	539			
Qy	224	ENSNQIPISLYSKLSLSEPLNTLSMTSAVQNTYTTTSCVTSSTSSLSNASPVMSSS	283			
Db	540	ASSSQAPSSLYTSTASSSSSTISSNQS--QESGYSQSGPIQSTTYSQN-NAQGLP----	591			

```

QY 284 YDOSSVHNRIPYOSPVSSSEAPGT-IMNGHGGGRSQOQLDTPKTTGP-----PSALPSV 337
Db 592 YERSTQTR-RYPSSSSSSQKDLTOAKNGFSSVQATQLOTTOSVEGATGSAVKSDSPST 650
QY 338 SSLP---STTSCTALLPSTSQHTG-----DLTSSPLSQLSSLSHQSLSAHAAL 385
Db 651 SSIPPLNETVSAASLLTTTHQSSSLGGLSHSEIPNNTTTTHQSSSTLSTQNTLSSTSS 710
QY 386 SSTSTHT--HAYVES-ASHQSGATSTTAATSVSSASGCVLSSSMNTANSICLGGTGA 442
Db 711 GRTSTLLTSTVESEANLHSSSTSTSTSTVSAPPPV-VSVSSSLNCGSSLGLSLGN 769
QY 443 SASSSSRAAPLVTSKAPNLPQGVPPILLHNOYLVGPGGLLPAYP--IVGYDELMQLS 500
Db 770 STVASTRSSVATTSKAPNLPQGVPPILLHNOYLVGPGGLLPAYP--IVGYDELMQLS 828
QY 501 RLPVDYIGIPFAAPTA-LASDRSLANNYPGVDVTKFGRGDSASAPATTPAQPOQSQQ 559
Db 829 RFLDYYSIPPTPTPLTCRGLSLANPYSGDLTKFGRGDASSAPATTLAQPOQNTQ 888
QY 560 THHTAQOFPVNPALPGYSYTGLPYIT---CMPSAFQYGTMP-VPPASAKQHGVLNLS-- 613
Db 889 THHTQOQFLNLPALPGYSYTGLPYITGVGPLESTFYGPAPFPVAPTSSKQHGVLNLSV 948
QY 614 TPTPPFOASGYGOGYSTG 633
Db 949 ASATPPQOPSGYSHGINTG 968

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RESULT 2

```

US-09-538-092-647
; Sequence 647, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 647
; LENGTH: 1140
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YMR317W
US-09-538-092-647

Query Match
Best Local Similarity 7.6%; Score 308.5; DB 4; Length 1140;
Matches 210; Conservative 131; Mismatches 352; Indels 221; Gaps 36;

QY 4 GTGS--STANVSCPSQLSVLGSFGELAPPKWANT-----SSQILDQLKAPSLGQFT 56
Db 210 GTTSDASKEVFSSTDSVLSLLS-----TSSPASSTISETLPFSSITLSITSPVSEAP 265
QY 57 TTPSTQNSTSHPTTTTSDWKLPSTQSSVLHDLFKSQPEPSPVLSQLSQROHQHQAQV 116
Db 266 SATSSSSVSSEASSTSSVSSEAPLATSSVVSS---EAPSTSSVVSSEAPSTSSSVSS 322
QY 117 TTPPPGLSPPSQAKUREST-----PGDSPVTNKLQLPSTTINIS-----V 160
Db 323 EISSTTSSSVSSEAPLATSSVSSEAPSTSSSVSS--EISSTTSSSVSSEAPLATSSVV 380

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QY 161 SVHQPOPKHIKLAKRRIPAPSKIPASAVEMPGSADVTGLNVQFALFEGFSEPSLSFSGSA 220
Db 381 SEAPSTSSSVSE--APSTSSSVSEAPSS---TSSSVSEISSTKSSVMSSEVSSA 435
QY 221 PSESNQIP---ISLYSKSLSEPLNTSLMTSAVQNSTYTTTSVITSCSLTSSLSNASP 277
Db 436 TSSLSVSEAPSAISSLASRLFSKNTSVT-----STLVATEASVITSSLSRPSSE 485
QY 278 VAMSSSYDOSSVHNRIPYOSPVSSSEAPGTIMNGHGGGRSQOQLDTPKTTGPPSPALPSV 337
Db 486 TLASNIIESSLT--GYNSTVITSTTSAASSTL-GSKVSSNSRMAITSKTSTSSDLKS 542
QY 338 SSIPSTSTCTALLPSTSQHTGDLTSSPLSQLSSSL--SSHQSLSLSAHAALSSSTSHTHASV 396
Db 543 SVIFGNSVTITSPASII---SLTASPLPSVMSDITSSSEASSISNLAASSAPSDNNSTI 599
QY 397 EASG-----SHQSATFTTAATSVSSASGVSLSL-----SNNTANSICLGG 439
Db 600 ASASLIVTKNSVSSIVSSITSETTNESNLATSTSLSNKATARSILSTSNATSAN 659
QY 440 TPASASSSSRAAPLVTSKAPNLPQGVPPILLHNOYLVGPGGLLPAYPIYGYDELO--- 496
Db 660 VPTGTFSMSSHTSVITPGFTSSASLAINSTVSSSLAG-----YFSTPESSP 709
QY 497 ---MLQSLPVDYIGIPPAAP-----TALASDRSLANNPY-PGVDVTKF 536
Db 710 TSTLVTSEAPSTVSMITTSAPFINNSTSARPSPTASFITESTSISVPLASGDT-- 767
QY 537 GRGDSAPAPATTPAQPOQSQQ---THHTAQOFPVNPALP-PGYSYTGLPYVTGMPSAP 592
Db 768 ---SSLAHNLATFSAPSTSSAQLVSKSTSSILVTPRIDRSGNSSTASRIATSLPN-- 822
QY 593 QYGPMTFVPP-----ASAKQ-----HCVNLSTPTPPF----- 619
Db 823 ---KITFVSSLSSTSAHARNIFNSTVLATAKQIETLTSTVNCNPPNNTKTVIVSRE 879
QY 620 -----QOASGYGOGYSTGYDLDLTQ-----GTAAGYSGYAGAGSSQ 656
Db 880 TTAIGTVTSCSGCTKRSITLITDIDASTVTCPEKEVTSTTSGDEAE--HTTSYK 937
QY 657 APN--KSAGSGPKGVSVSSSTTGLPDMTGVSVNKTQTQFDKGFHAGTTP-----PFSLP 709
Db 938 ISNFTSTFSESGFKDMKTSQETKAKPGSETVRSSSSFVEK-----TSPTTKASPTSP 991
QY 710 SVLGSSTG--PLASGAAGYAPPPFLLHLPALHQAQPHSQLHHLHPDAQSGSORSQSSSL 767
Db 992 SESKAAGNTSVATNASPTSP-----SESQGTGSTVEGA- 1026
QY 768 QPKSQASKPAYGNS 781
Db 1027 --KSKSTKNSGV 1038

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RESULT 3

```

US-09-538-092-330
; Sequence 330, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 330
; LENGTH: 1306
; TYPE: PRT

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Db 908 TTDASQDSSTSDSGTSTSDTTSDSSNSTSTSDSSGLSQTSPDSSSASDSMTTVD 967
Qy 554 QOSQ-----SQTHTAQPPFNALP---PGSYTGL-----PY-- 585
Db 968 DASTETPYFVLENLWNETVYSENPFYITIPNKEFGALTATMTCQRNDSSQPFVLL 1027
Qy 586-----TGMPSA-FQGP-TMFVPPASAKQGVNL----- 612
Db 1028 KESNCLTEFGKNGAYSASVSFNPMTSFVPATGTVEFLINVTNRASGESASHIFTMNVVLP 1087
Qy 613--STPTTFFQAGVGQHGYSYGYDDLTQGT-----AAGDYKGGYAGSSQAP 658
Db 1088 TTTTETPP-TTVSSDDAGKGTGTGATCGGTGCGSGSANTLTSGDAVRTTSGSGSQ 1146
Qy 659 NKSAGSGFGKGVSSSSTTGLPDMTGVSYNKTOTFDKQGFHAGTTPPFSLPSVLGSGCPL 718
Db 1147 SSTGSGAGSGTTASGSGSGSGSGTGS-----DGVNSGK-----TTALN 1185
Qy 719 ASGAAPGYAPPPFHLHPAHQPHSOLLHHLLPQDAQSGSGQRQSPSS-LQPKQASKPA 777
Db 1186 GDGTGSGTATTPGSHLGDG-----GSTSGSGSDSGSGSVSTKSSGSDT 1230
Qy 778 YGNS 781
Db 1231 SGSS 1234

RESULT 7
US-09-538-092-1081
; Sequence 1081, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 1996-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-12-7,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 1081
; LENGTH: 2090
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P35658
US-09-538-092-1081

Query Match 7.1%; Score 286.5; DB 4; Length 2090;
Best Local Similarity 23.2%; Pred. No. 1.5e-10;
Matches 215; Conservative 104; Mismatches 349; Indels 257; Gaps 43;

Qy 36 ANITSSQILDQKAPSLGQFTTTPSTQNSTSHPTTISWD-----LKPPTS 82
Db 965 ASLSRSFLSRQYEDLDEVSSTSVSQSUESEDARTSCDKDEAVVQAPRHAPVYRTPSI 1024
Qy 83 QSSVL-----SHLDFKSPQ-----EPSPVLSQSRQHQSOQAVT--VPPPGL 123
Db 1025 QPSLLPHAAPFAKSHLVHSGSPGVNCTSVATSASKIIPQGDSTMLATKTVKCAPSPSH 1084
Qy 124 E-SPPSQ---AKLRETPGSPSTVNKLLQLPSTTIENISVNHQPOPKHKLAKRIPP 179
Db 1085 PISAPQQLAAALRRQMASQAPA-VNTLITE---STLXNV-----PQVNVVQELKNP 1132
Qy 180 A-----SKIPASAVEMPGS--ADVTGLNVQFQAL-----EFGSEPSLSEFGSAPSEN 225
Db 1133 ATPSTAMGSSVPYFTAKTPHPVLTPVAANOAKQGLNSLKLPSGFTPASQGLSSGDKASG 1192
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Qy 226 SNQIPISLYSK-----SLSEPLNLTSLMST-----AVQNSTYTTSTVITSCSLTSSSLNSASP 277
Db 1193 TAKLETAVTSTPSASGQSKPFPSPSGTGPNFGIITPTPSNFTAAQAGATPSTKESQ 1252
Qy 278 VAMSSSYDQSSVNHRIPIQSPVSSSESAPGTIMHGGGRSQOQLDTPKTTGPPSALPSV 337
Db 1253 DAFSSGGGSRPSVEAIPESPSPGITSANT-----TPEEPAA---S 1291
Qy 338 SSLPSTTCTALLPSTSOHTGDLTSSPLSOLSSSLSHQSSLSAHAAL----- 385
Db 1292 SSRPVAESGIAL--STTSSKLETPPKLGGELLFPSSLAGETLGSFGLRVQQAODSTKPT 1349
Qy 386--SSSTS-----HTHASVESASHSQSATFSTAATSVS 417
Db 1350 NKASSTSLTSTQPTKTSGVPGFNFAPVPLGKHTEPPTVSSATTSVA--PPAATSTSS 1407
Qy 418 SASGCVLSMMYANSLCGLTGPASASSSSSRRAAPLVTSKAPPNLP---QGVPPLLHN 474
Db 1408 TAVFGSLPVTSSAGSGVIFSGGTSLSAGKTSFSGSQQTNSTVPPSAPPTTAATPLPTS 1467
Qy 475 QYLVGPGCLL-----PAYPI-YGYDELOQLQSLRPVDYGYIPPAAPTALASRDRSLANNP 528
Db 1468 FPTLSFGSLSSATTPSLPMSAGRSTEEATSSALPEKPGDSEVSASASLLEEQSAQLP 1527
Qy 529 YPGDVTKFGRGDSASAPATTPAQPOQSQSOQTHHTAQPPFVNPALPPGYSTGLPYTYGM 588
Db 1528 QAPPQT-----SDSVKKEPVL--AQPAVNSNGTAASSTSLV-----ALSAEATPATTV 1574
Qy 589 PSAPQYQPTMFVPPASA-----KQGVNL-----STPTP-----PFQ 620
Db 1575 PDA-----RTEAVPPASSFVPGQTAVTAAAISSAGPVAVETSTPIASSTTSIVAPGPSA 1630
Qy 621 QASGYG-----QHGYSTGYDDLTQGTAAADYSKG--GYAGSSQAPNKSAGSG 665
Db 1631 EAAAFGVTVSGSVFAOPPAASSSSAFNQNTNNTATAPSATPVFQVAAATAPS-LFGQQ 1689
Qy 666 PGKGVSVSSSTTGLPDMTGVYNNKTQTFDKGFHAGTTPPPF--SLPSVLGST----- 715
Db 1690 TGSTASTAAAT--PQVSSS-----GF---SSPAFGTTAPGVGOTTTFQASVF 1732
Qy 716 GPLASGAAP--GYAPPPFHLHPAHQPHSOLLHHLPQDAQSGS--GQRSQPSLQPKS 771
Db 1733 GQSASSAASVFSFQPGFSSV-PAFGQPASS-----TPTSTSGSVFCAASSTSSSSFS 1785
Qy 772 -----QASKPAYGNP 782
Db 1786 FGSSPNVTGGGLFGQSNAPAFQSP 1810
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RESULT 8

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US-09-134-001C-4463
; Sequence 4463, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GFC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4463
; LENGTH: 2137
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4463
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Query Match 7.0%; Score 282.5; DB 3; Length 2137;

	Best Local Similarity	21.3%;	Pred. No. 2.9e-10;	
	Matches	157;	Conservative	108;
			Mismatches	319;
			Indels	153;
			Gaps	16;
QY	5	TGSGTAIVNCSPQSLSSVLSGFGELAPPKMANIT	SQILDQLK-APSLGQFTTPTSTQ	63
DB	1417	TSVSDSTSTSDSASASTSES	DSERASTSLSGSTSTSDSTSTSDSTSTSDSTSVSES	1476
QY	64	NSPSHPTTTTWSDLKPTTSQSSVLSHLDFKSP	QEPGPVLSQLSQRQHQHQAQVTPPPGL	123
DB	1477	NSPS---TSISELSSTSVSDSTSTSDSAS---	TSTSVSDSDSASTSSSESYST---	1525
QY	124	ESPPQAKLRSTPGDPSPTVNKLLOLPST---	-----TIENISVSVHQ	164
DB	1526	-----SDSESTSTSDSASASTSVSESNSTSL	SGSTSTSVSDSTSTSDSASASTSE	1581
QY	165	PQPKHKLAKRIRPPAKKIPASAVE	PGSA---DYTGILNVQFCALEFGSEPSLSRFGSA	220
DB	1582	SDSDASASTSSSESYSTSVSDSTSDASTSES	ASTSTSVSDSNASTSESTSTSLSDSTSM	1641
QY	221	PSSENSNQIFISLYKSLSPLNTSLMTSAVQNS	TVTTSVITSCSLTSSLSNAPSAM	280
DB	1642	STSDASASTSESDDSDASTSLDSTSTSVSEST	STSTSVSNASTSTSLSDSRSTSL	1701
QY	281	SSSYDQSSVHNRIPIQSPVSSSESAPOTIMN	HGGGRSQOTLDPKTTGPPSALPVSVSL	340
DB	1702	SDSTSTSTSES---GSTSTESDSDASTSLSE	STSGSTSTSDSTSTSDSASTSMVS	1756
QY	341	PSSTCTALLPSTSQHTGDTLTSPLSQLSSLS	HQSLSAHAALSSSTSHTHASVESAS	400
DB	1757	DSNRASTSLSDSTSTSVSDSTSDASTSE	ASTSTSTRESESTASTSLSEST---	TSVS 1810
QY	401	SHQSSATFSTAATSVSSSAGSVLSSSMTAN	SLCLGGTPASASSSSSRAAPLVTSGKA	460
DB	1811	DSTSTSDSASTSTESDSESTSLSESTSVS---	DSSTASSTASASTSTSVSDNSA	1869
QY	461	PPNLPGQVPPLHNQYLVGPGGLLPAYPIY	GYDELOMLQGRLPVDYIGIPFAAPTALASR	520
DB	1870	STSLSGSTSTSVSDSTSTSTA-	-----SASTSTSES	1900
QY	521	DRSLANNPYG-----DVTKFRGDSASPA---	PATTPAQPOOSQOHTHTTAQQFPVN	570
DB	1901	DSDSASTSLSGSTSTSDSTSTSDSTSDAST	STSESASTSTSVSESDSESTSVSE---	1955
QY	571	PALPPGYSYTGLPYYTGMPSAFYGPTMFV	PPASAKQGVNLSTPTPPFOAASGYGQHG	630
DB	1956	-----	-----SSSTSVSDSTSTSTSESASTSESE	1981
QY	631	STGYDDLTOGTAAGDYSKGGVAGS-----	---SQAPNKASAGGPKGVSV---	671
DB	1982	ST-----SESTSVSESSSTISDSSSTST	SMSTGETFTSQSPINSESQFIGDLSLEDTV	2036
QY	672	VSSSTTGLPDMTGSVYN	688	
DB	2037	TQSKNTNMLNKTGKDYD	2053	

```

RESULT 9
US-09-579-181-2
; Sequence 2, Application US/09579181
; Patent No. 6365372
; GENERAL INFORMATION:
; APPLICANT: Chrvivia, John
; APPLICANT: Yaciuk, Peter
; TITLE OF INVENTION: SNF2 Related CBP Activator Protein (SRCAP)
; FILE REFERENCE: 16153-4247
; CURRENT APPLICATION NUMBER: US/09/579,181
; CURRENT FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/136,620
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2972

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; TYPE: PRT
; ORGANISM: Human
US-09-579-181-2

Query Match      6.7%; Score 273.5; DB 3; Length 2972;
Best Local Similarity 24.1%; Pred. No. 1.9e-09;
Matches 217; Conservative          94; Mismatches 323; Indels 265; Gaps 45;

QY   1  MAPGTGSTAVNGCSPOSLSVLG--SGFG-----ELAPPKMANII-----SSQI 43
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB   878 LQPNSGS-----LPQVLEPSLGVISGTSRPFPTTSLSKPTPPAVRLSPAPPGSSSL 930
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY   44 LDQLKAPSLGQFTTTTPTGTONSNSHPTTTTSDWLKPPTSQSSLHSLDFKSQPEPSPVL 103
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB   931 LKPLTVPPGYTFPPAAATTTTATATTAVPAFTPAPQLILSP--DMQARLPSEGEWS 989
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
QY   104 --QLSORQQHQ-----SQAVTVPPPGLSEFPQAKURESTPDGDSPTVNKLQLPSTTI 155
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:
DB   990 IGQLASLAFQVANAGGSKFLTFOIQNKLTLTGAQVRQLAVGOP----RPLQMPTMW 1044
    :|||:|||||:|||||:|||||:|||||:|||||:
QY   156 EN---ISVSVHQ-----POPKHIKLAKRRIPPAKIPA-----185
    :|||:|||||:|||||:|||||:|||||:|||||:
DB   1045 NNTGVXIVVRQAARDGLTPVP-----PLAPAPRPSSGLPVLNPRPTLTGRLTPTLGT 1101
    :|||:|||||:|||||:|||||:|||||:|||||:
QY   186 SAVEMPGSADVTGLNVQFALGFEGSEPSLSEFGASPSENSNQIPISIYSKSLSEPLNTS 245
    :|||:|||||:|||||:|||||:|||||:|||||:
DB   1102 ARAPMPTTLVRPL-----LKVHSPSPSVASAPGA-----APL-----TISPLHPV 1145
    :|||:|||||:|||||:|||||:|||||:|||||:
QY   246 LSMTS-----AVONSTYTTSVIITSCSLTSSLSNASPVAMSSSYD-QSSVHNRIYOSP 298
    :|||:|||||:|||||:|||||:|||||:|||||:
DB   1146 SSLPCPASSMPPIPNSGPLASPVBS--STVSVPLSSSLPISVPTTLPAPASAPLTIPISAP 1203
    :|||:|||||:|||||:|||||:|||||:|||||:
QY   299 VSSSESAPGTMINGGGGRSQOTLDT-----PKTTGPPSALPSVLSLPTTCTALLP 351
    :|||:|||||:|||||:|||||:|||||:|||||:
DB   1204 LTVASGPALL-----TSVTPPLAPVVPAAPGPPSLQPSGAS-----P 1244
    :|||:|||||:|||||:|||||:|||||:|||||:
QY   352 STSOHTGDLTSSPQLSSLSHSQSLSAHAALSSTSTSHTHASVESASSHOS--SATFS 409
    :|||:|||||:|||||:|||||:|||||:|||||:
DB   1242 SASALTGLLATAP-----SLSSQOT--PGHPLLAPT-----SSHVGLUNSTVA 1283
    :|||:|||||:|||||:|||||:|||||:|||||:
QY   410 TAATSVSASSGVVS-LSSSMNTANSLCLGCTPASASSSRRAAPLVTS GKAPPN---LP 465
    :|||:|||||:|||||:|||||:|||||:|||||:
DB   1284 PACSPVLVPAGALASPFPSAPNPAPAQASLLAPAS-SASQALATFLAPMA-APQTAILAP 1344
    :|||:|||||:|||||:|||||:|||||:|||||:
QY   466 QGVPPILLNQYLVGPGGLPAYPIGYDELOMQRLPVDYIGVIPFAAPTALASDRSLA 525
    :|||:|||||:|||||:|||||:|||||:|||||:
DB   1342 SPAPPLAPLVLAPSPGAAPV-----LASSQTEV-----PVMAPS--STPGTSLA 1384
    :|||:|||||:|||||:|||||:|||||:|||||:
QY   526 NNYPGCVTKRGDASAPATAIPA-----SQPOOSQOETHTAQQPFVN 570
    :|||:|||||:|||||:|||||:|||||:|||||:
DB   1385 -----SASGVPAPTPVLAPSTQTMLPAPVPSPLSPASTQTIALALPALA 1421
    :|||:|||||:|||||:|||||:|||||:|||||:
QY   571 PALPPGYSVTGLPYTGMPSAFQYGF-----TMFVPPASA-----KHGVNL 613
    :|||:|||||:|||||:|||||:|||||:|||||:
DB   1430 PTLGGSSPSQTLSLGTGNPQ-----GPFPTQTLSLTPASSLVPTPAQTLSLAGPPLGPTQG 1481
    :|||:|||||:|||||:|||||:|||||:|||||:
QY   614 ----TPTPPFOAQSGYGQHGYSTGYDDLTQGTAAAGDYSGKGAGSQAENKAGSGSPGKG 669
    :|||:|||||:|||||:|||||:|||||:|||||:
DB   1486 TLSLAPAPPLAPASVPVGAFAHT-----LTLAPASASSALLAPA-SVQTUTLSAPVPVTLG 1544
    :|||:|||||:|||||:|||||:|||||:|||||:
QY   670 VSVSSTTGLPDMWTGVSYNKTQTFDKQGHACTPPPPFSLPSVLSTGTPLASGAAGYAPP 729
    :|||:|||||:|||||:|||||:|||||:|||||:
DB   1541 PAQAQTALAP-----ASTQSPASQASSLVVS--ASGAAP--LPV 1571
    :|||:|||||:|||||:|||||:|||||:|||||:
QY   730 PFLHLIPAHQPHSOLLHHHLFDQAQSGGQRSGQSSLQ-----PKSQASKPAYGNSPYW 784
    :|||:|||||:|||||:|||||:|||||:|||||:
DB   1577 TWVSRLPVSKDE-----PDTLTRSGPTSPFSTATSFQGPFRPRQPPPPRSFFY 1626
    :|||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
US-09-579-181-1
; Sequence 1, Application US/09579181
; Patent No. 6365372
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RESULT 10
US-09-579-181-1
; Sequence 1, Application US/09579181
; Patent No. 6365372

Matches 204; Conservative 141; Mismatches 370; Indels 273; Gaps 43;

Qy 2 APGTGSSTAV-----NSCSPQSLSSVLGSGFGLAPPKM---AN 37
 Db 813 APTTSSQAVLESTQGVSOVAPAEVPAVQAQPTPTTLASSVDSAHSDVASGMSDGNEN 872
 Qy 38 ITSS-----QILDQLKAPSLGQFTTTP-----STQNSTSHPTT 71
 Db 873 VPSSSGRHEGRTTKRHYKRSVRSRHEKTSRPKLRILNVSNKGDVVECCOLETHNRKV 932
 Qy 72 TTSMDL--KPTSSQSVLSHLDFKQSPSPVLSQ----LSQROHQSOQAVTVP---PG 122
 Db 933 TFKFDLGDNDPEEATIMVNDNFILAIERESFVDQVREIIEKADMLSEDSVSEPEGDQ 992
 Qy 123 LES-----FPSQAKLRESTPGDSP--STVNKLQLPSTTIENISVS-----VHQPOPK 168
 Db 993 LESLQGGDDYGFSGSQKLEGEFKQIPASSMPQIQIGTSSLTQVHVHAGRRFIVSPVPE 1052
 Qy 169 HIKLAKRIPPA---SKIPASAVEMPGSADVTGLNVQFGALEFGSEPSLSFEGSAPSEN 225
 Db 1053 S-RLRESKVFPSEITDTVAASTAQSP-----GMNLSHSASSLSLQQAFAFSELRAQMTEG 1105
 Qy 236 SNQIPISLYSKLSEP--LNTSLMTSAVQNSTYTTVITSCSLTSSLSNASPVAMSSSY 284
 Db 1106 PNTAPPNFSHTGTPFPVVPFLLSSITAGVPTTAATAAPVPA-----TSSPPNDISTSV 1157
 Qy 285 DQSSVHNRIQSPVSSSESAPGTMNGHGGRSQOITLDTPTKTGPP-----SALPS 336
 Db 1158 IQSEV--TVPTTEGIAGVATSGVVTSG-----GLPIPVSESPVLSVSVSIIPA 1207
 Qy 337 VSSLPSTT-----SCTALLPS-----TSQHTGDLTSSP----- 364
 Db 1208 VVSIITSPSLQVPTSTSEIVVSSSTALYPSTVTSATSAGGSTATPGKPPAVVSOQAA 1267
 Qy 365 -----LSQSSLSHSHQSSLSAHLSSSTSH---THASVESA-----SSHQSATP 408
 Db 1268 GSTTVGATLTSVSTTSPFSTASQLSITLSSSTSTPTLAETVTVVSAHSLDKTSHSTGL 1327
 Qy 409 STAATSVSSSASSGVSSSSMNTANSL-----CLGCTPASASSSSRAAPLVTS--GKA 460
 Db 1328 AFSLAPSSSSSPGAGVSSYISQGGHLPLVPSVIASTPILPQAGTSTPFLPQVPSI 1387
 Qy 461 PP-----NLPQGVPPILLHNQYLVGPGGLPAYP-----IYGYDELOMLQS 500
 Db 1388 PPLVQPVANVPAVQOTLIHSQ---POPALLPNQPHTHCPEVDSDTQPKAPGIDDIKTEE 1444
 Qy 501 RLPVDY-----GIP--FAAPTALASDRSLANNPYPGD 532
 Db 1445 KRLSLSHSSGQASHVSLETSLVIESVTPTGPTTAVAPSKLLTSTTCLPP--- 1500
 Qy 533 VTKEGRGDSAP-APATTPAQOQSQTHHTAQOPFVNPALPPGYSVTGLPYVTGMPSA 591
 Db 1501 -TNLPLGTVALPVTVPTGQVSTPVSTT--TSQVKPGTAPSKPLTKAPVLVPGTELPA 1558
 Qy 592 FOYGTMFVPPASAKQHGVLNLTSTPPPPQASGYGQHGYSFGYDGLTQGTAGDYSGGY 651
 Db 1559 TL--PSEQLPFP--GPSLTQSOQPLEDLAQLRRLTSP--EXITVTSVAVGPVMA-- 1608
 Qy 652 AGSSQAPN--KSAGSGPKGV-----VSSSTTGLPDM-----TGSVY 687
 Db 1609 -----APTAITEAGTQPKGVQVKEGVLATSSGAGVFKMRFPQVSVAAADGAKGK-- 1661
 Qy 688 NKTOTFDKQGHACTPPFPFSLPSVLGSTGTPLASGAAFGYAPPPHLILPAHQPHSOLLH 747
 Db 1662 NKSEDAKSVHEST-----SSSVLSSSSPESTLV-----KPEPNGITIPGISSDVPESA 1713
 Qy 748 HHLPDQAGSQGQSQSPSSLPKFSQAK 775
 Db 1714 KTTASEAKSDGTQPKVGRFQVTTTANK 1741

RESULT 14
 US-09-854-856-26

; Sequence 26, Application US/09854856
 ; Patent No. 6541252
 ; GENERAL INFORMATION:
 ; APPLICANT: Walke, D. Wade
 ; APPLICANT: Hilbun, Erin
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides
 ; FILE REFERENCE: LEX-0178-USA
 ; CURRENT APPLICATION NUMBER: US/09/854,856
 ; CURRENT FILING DATE: 2001-05-14
 ; PRIOR APPLICATION NUMBER: US 60/206,015
 ; PRIOR FILING DATE: 2000-05-19
 ; NUMBER OF SEQ ID NOS: 64
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 26
 ; LENGTH: 2064
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)...(2064)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 ; US-09-854-856-26

Query Match 6.4%; Score 260.5; DB 4; Length 2064;
 Best Local Similarity 20.6%; Pred. No. 8.6e-09;
 Matches 204; Conservative 141; Mismatches 370; Indels 273; Gaps 43;

Qy 2 APGTGSSTAV-----NSCSPQSLSSVLGSGFGLAPPKM---AN 37
 Db 845 APTTSSQAVLESTQGVSOVAPAEVPAVQAQPTPTTLASSVDSAHSDVASGMSDGNEN 904
 Qy 38 ITSS-----QILDQLKAPSLGQFTTTP-----STQNSTSHPTT 71
 Db 905 VPSSSGRHEGRTTKRHYKRSVRSRHEKTSRPKLRILNVSNKGDVVECCOLETHNRKV 964
 Qy 72 TTSMDL--KPTSSQSVLSHLDFKQSPSPVLSQ----LSQROHQSOQAVTVP---PG 122
 Db 965 TFKFDLGDNDPEEATIMVNDNFILAIERESFVDQVREIIEKADMLSEDSVSEPEGDQ 1024
 Qy 123 LES-----FPSQAKLRESTPGDSP--STVNKLQLPSTTIENISVS-----VHQPOPK 168
 Db 1025 LESLQGGDDYGFSGSQKLEGEFKQIPASSMPQIQIGTSSLTQVHVHAGRRFIVSPVPE 1084
 Qy 169 HIKLAKRIPPA---SKIPASAVEMPGSADVTGLNVQFGALEFGSEPSLSFEGSAPSEN 225
 Db 1085 S-RLRESKVFPSEITDTVAASTAQSP-----GMNLSHSASSLSLQQAFAFSELRAQMTEG 1137
 Qy 226 SNQIPISLYSKLSEP--LNTSLMTSAVQNSTYTTVITSCSLTSSLSNASPVAMSSSY 284
 Db 1138 PNTAPPNFSHTGTPFPVVPFLLSSITAGVPTTAATAAPVPA-----TSSPPNDISTSV 1189
 Qy 285 DQSSVHNRIQSPVSSSESAPGTMNGHGGRSQOITLDTPTKTGPP-----SALPS 336
 Db 1190 IQSEV--TVPTTEGIAGVATSGVVTSG-----GLPIPVSESPVLSVSVSIIPA 1239
 Qy 337 VSSLPSTT-----SCTALLPS-----TSQHTGDLTSSP----- 364
 Db 1240 VVSIITSPSLQVPTSTSEIVVSSSTALYPSTVTSATSAGGSTATPGKPPAVVSOQAA 1299
 Qy 365 -----LSQSSLSHSHQSSLSAHLSSSTSH---THASVESA-----SSHQSATP 408
 Db 1300 GSTTVGATLTSVSTTSPFSTASQLSITLSSSTSTPTLAETVTVVSAHSLDKTSHSTGL 1359
 Qy 409 STAATSVSSSASSGVSSSSMNTANSL-----CLGCTPASASSSSRAAPLVTS--GKA 460
 Db 1360 AFSLAPSSSSSPGAGVSSYISQGGHLPLVPSVIASTPILPQAGTSTPFLPQVPSI 1419
 Qy 461 PP-----NLPQGVPPILLHNQYLVGPGGLPAYP-----IYGYDELOMLQS 500
 Db 1420 PPLVQPVANVPAVQOTLIHSQ---POPALLPNQPHTHCPEVDSDTQPKAPGIDDIKTEE 1476

Qy	501	RLPVDY	-----GIP--FAAPTALASDRSLANNPYPGD	532
Db	1477	KLSLSEHSSGAQHASVLSLSTLSTVTPGIPTTAVAPSKLLTSTTCLPP	-----	1532
Qy	533	VTKFGRGDSASP-APATTAPQOQSQOHTHTAQOFPVNPALPPGYSTGLPYTGMPSA	591	
Db	1533	-TNLPLGTVALPVTVPVTPQGVSTPVT--TSGVKFGTAPSKPPLTKAPVLPGVGTLPAG	1590	
Qy	592	FQYGTMTFVPASAKOHGYNLSTPTPPFOQASGYQHGYSTGYDDLTQGTAAAGDYSKGY	651	
Db	1591	TL--PSEQLPFPF-----GSLTQSQOPLDLDLQARTLSP--EXITVTSAGVPVSM--	1640	
Qy	652	AGSSQAPN--KSAGSGPGKGV-----VSSSTTGLPDM-----	TGSVY	687
Db	1641	-----APTAITEAGTQPKGVSVKQEGPVLATSSGAGVFKMGRFQVSVAAADGAQKEGK--	1693	
Qy	688	NKTQTFDKQGFHAGTPTPLPSVLSTGTLASGAAPGYAPPFLHILPAHQPHSOLLH	747	
Db	1694	NKSEDAKSVHFESST-----SESVLSSSPESTLV-----KPEPNGITIPGISDVPESA	1745	
Qy	748	HHLPODAQSGSGORSQPSLSQPKSOASK	775	
Db	1746	KTTASEAKSDTGQPTKVGRFQVTTTANK	1773	

RESULT 15

US-09-854-856-10

Sequence 10, Application US/09854856

Patent No. 6541252

GENERAL INFORMATION:

APPLICANT: Walke, D. Wade

APPLICANT: Hilbun, Erin

APPLICANT: Donoho, Gregory

APPLICANT: Turner, C. Alexander Jr.

TITLE OF INVENTION: No. 6541252el Human Kinases and Polynucleotides

FILE REFERENCE: LEX-0178-USA

CURRENT FILING DATE: 2001-05-14

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 64

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10

LENGTH: 2092

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)...(2092)

OTHER INFORMATION: Xaa = Any Amino Acid

US-09-854-856-10

Query Match

Best Local Similarity 20.6%; Pred No. 8.8e-09;

Matches 204; Conservative 141; Mismatches 370; Indels 273; Gaps 43;

Qy

2

APGTGSSTAV-----NCSQPSQSLSSVLGSGFCELAPPKM---AN

37

873

APTTSSQAVLSTQGVSAPEAVPAVAQPOATQPTTLASVDSAHSDVAGSMGDGNE

932

Db

38

ITSS-----QILDQKAPSLGQPTTP-----STQONSSTHPTT

71

Qy

933

VPSSSGRHEGRTTKRHYKRSVRSRHEKTSRPKRLNVNKGDRVVECCOLETHNRQW

992

Db

72

TTSDWL--KPPTSQSVLGHDFKSOPEPSVLQ-----LSQROHQSOAVTVP--PG

122

Qy

993

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LES-----FPSQAKRESTGDSPT-STVKKLLQLPSTTIENISV-----VHQPOPK

168

Qy

1053

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1112

Db

Search completed: January 31, 2005, 17:47:58

Job time : 29 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 31, 2005, 17:42:12 ; Search time 71 Seconds
(without alignments)
3999.626 Million cell updates/sec

Title: US-10-509-307-1

Perfect score: 4055

Sequence: 1 MAPGTGSTAVNSCSQSLG.....LQPKSQASKPAYGNSPYWTN 786

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1608061 seqs, 361289386 residues

Total number of hits satisfying chosen parameters: 1608061

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1536	37.9	363	10	US-09-946-374-72
2	1536	37.9	363	13	US-10-052-586-252
3	1536	37.9	363	14	US-10-174-590-252
4	1536	37.9	363	14	US-10-176-758-252
5	1536	37.9	363	14	US-10-175-737-252
6	1536	37.9	363	14	US-10-174-581-252
7	1536	37.9	363	14	US-10-176-483-252
8	1536	37.9	363	14	US-10-176-749-252
9	1536	37.9	363	14	US-10-176-914-252
10	1536	37.9	363	14	US-10-176-915-252
11	1536	37.9	363	14	US-10-173-706-252
12	1536	37.9	363	14	US-10-175-738-252
13	1536	37.9	363	14	US-10-175-752-252

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15	1536	37.9	363	14	US-10-176-757-252	Sequence 252, App
16	1536	37.9	363	14	US-10-176-913-252	Sequence 252, App
17	1536	37.9	363	14	US-10-180-552-252	Sequence 252, App
18	1536	37.9	363	14	US-10-180-557-252	Sequence 252, App
19	1536	37.9	363	14	US-10-173-700-252	Sequence 252, App
20	1536	37.9	363	14	US-10-174-572-252	Sequence 252, App
21	1536	37.9	363	14	US-10-174-579-252	Sequence 252, App
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23	1536	37.9	363	14	US-10-174-588-252	Sequence 252, App
24	1536	37.9	363	14	US-10-175-739-252	Sequence 252, App
25	1536	37.9	363	14	US-10-175-740-252	Sequence 252, App
26	1536	37.9	363	14	US-10-175-743-252	Sequence 252, App
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29	1536	37.9	363	14	US-10-176-747-252	Sequence 252, App
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33	1536	37.9	363	14	US-10-176-992-252	Sequence 252, App
34	1536	37.9	363	14	US-10-176-993-252	Sequence 252, App
35	1536	37.9	363	14	US-10-184-658-252	Sequence 252, App
36	1536	37.9	363	14	US-10-176-991-252	Sequence 252, App
37	1536	37.9	363	14	US-10-173-695-252	Sequence 252, App
38	1536	37.9	363	14	US-10-173-697-252	Sequence 252, App
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41	1536	37.9	363	14	US-10-174-585-252	Sequence 252, App
42	1536	37.9	363	14	US-10-174-586-252	Sequence 252, App
43	1536	37.9	363	14	US-10-175-747-252	Sequence 252, App
44	1536	37.9	363	14	US-10-176-481-252	Sequence 252, App
45	1536	37.9	363	14	US-10-176-485-252	Sequence 252, App

ALIGNMENTS

RESULT 1
US-09-946-374-72
; Sequence 72, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C1
; CURRENT APPLICATION NUMBER: US/09/946.374
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749

[illegible]


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; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
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; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908
; PRIOR APPLICATION NUMBER: 60/089908

Query Match 37.9%; Score 1536; DB 13; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQTTTPTSTOON 64
Db 9 NSVILRICSFILLLKSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQTTTPTSTOON 68
QY 65 STSHPTTTTSDWKPTTSSQSSVLSHLDKSPSPVLSQLSORQOHSQAVTVPPGLE 124
Db 69 STSHPTTTTSDWKPTTSSQSSVLSHLDKSPSPVLSQLSORQOHSQAVTVPPGLE 128
QY 125 SPFSQAKLRESTPGDSPSTVNKLLQLPSTTTIENISVSVHQPOPKHKLAKRIPPASKIP 184
Db 129 SPFSQAKLRESTPGDSPSTVNKLLQLPSTTTIENISVSVHQPOPKHKLAKRIPPASKIP 188
QY 185 ASAVEMPGSADVTGLNVQFGLPGESEPSLSFSGAPSESENNOIPISTYKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLPGESEPSLSFSGAPSESENNOIPISTYKSLSEPLNT 248
QY 245 SLSTSAVQNSTYTTSVTTSCTSTSSLSNSAPSVAMSSSYDQSSVHNRIPIYQSPVSSSES 304
Db 249 SLSTSAVQNSTYTTSVTTSCTSTSSLSNSAPSVAMSSSYDQSSVHNRIPIYQSPVSSSES 308
QY 305 APGTIMNGHGGGRSQOQLDT 324
Db 309 APGTIMNGHGGGRSQOQLDLS 328

RESULT 3
US-10-174-590-252
; Sequence 252, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-252

Query Match      37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFIPLLKSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 68
Qy 65 STSHPTTTTSDWLKPPPTSSQSVLSHLDFKQPEPSVLSQSRQHQSOAVTVPPPGLE 124
Db 69 STSHPTTTTSDWLKPPPTSSQSVLSHLDFKQPEPSVLSQSRQHQSOAVTVPPPGLE 128
Qy 125 SFPQAKLRESTPGDSPSTVTKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIIPPASKIP 184
Db 129 SFPQAKLRESTPGDSPSTVTKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIIPPASKIP 188
Qy 185 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSEFGSAPSSSENSNOIPISLSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSEFGSAPSSSENSNOIPISLSKSLSEPLNT 248
Qy 245 SLWMTSAVQNSTYTTTSSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLWMTSAVQNSTYTTTSSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
Qy 305 APGTIMNGHGGRSQQTLD 324
Db 309 APGTIMNGHGGRSQQTLD 328

RESULT 4
US-10-176-758-252
; Sequence 252, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-252

Query Match      37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFIPLLKSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 68
Qy 65 STSHPTTTTSDWLKPPPTSSQSVLSHLDFKQPEPSVLSQSRQHQSOAVTVPPPGLE 124
Db 69 STSHPTTTTSDWLKPPPTSSQSVLSHLDFKQPEPSVLSQSRQHQSOAVTVPPPGLE 128
Qy 125 SFPQAKLRESTPGDSPSTVTKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIIPPASKIP 184
Db 129 SFPQAKLRESTPGDSPSTVTKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIIPPASKIP 188
Qy 185 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSEFGSAPSSSENSNOIPISLSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSEFGSAPSSSENSNOIPISLSKSLSEPLNT 248
Qy 245 SLWMTSAVQNSTYTTTSSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLWMTSAVQNSTYTTTSSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
Qy 305 APGTIMNGHGGRSQQTLD 324
Db 309 APGTIMNGHGGRSQQTLD 328

RESULT 5
US-10-175-737-252
; Sequence 252, Application US/10175737
; Publication No. US20030013153A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C50
; CURRENT APPLICATION NUMBER: US/10/175,737
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-252

Query Match      37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFIPLLKSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 68
Qy 65 STSHPTTTTSDWLKPPPTSSQSVLSHLDFKQPEPSVLSQSRQHQSOAVTVPPPGLE 124
Db 69 STSHPTTTTSDWLKPPPTSSQSVLSHLDFKQPEPSVLSQSRQHQSOAVTVPPPGLE 128
Qy 125 SFPQAKLRESTPGDSPSTVTKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIIPPASKIP 184
Db 129 SFPQAKLRESTPGDSPSTVTKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIIPPASKIP 188
Qy 185 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSEFGSAPSSSENSNOIPISLSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSEFGSAPSSSENSNOIPISLSKSLSEPLNT 248
Qy 245 SLWMTSAVQNSTYTTTSSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
Db 249 SLWMTSAVQNSTYTTTSSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIQSPVSSSES 308
Qy 305 APGTIMNGHGGRSQQTLD 324
Db 309 APGTIMNGHGGRSQQTLD 328

RESULT 6
US-10-176-758-252
; Sequence 252, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363

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[illegible]


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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17

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; PRIOR APPLICATION NUMBER: 60/089653
Query Match 37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKXANITSSQILDQKAPSLGQTTTPTSTQON 64
Db 9 NSVLLRICSFPLKSSVLGSGFGLAPPKXANITSSQILDQKAPSLGQTTTPTSTQON 68

Qy 65 STSHPTTTTSDLKPPPTSQSSVLSHLDFKSPSPVLSQSLSQOQHQSOAVTTPPPGLE 124
Db 69 STSHPTTTTSDLKPPPTSQSSVLSHLDFKSPSPVLSQSLSQOQHQSOAVTTPPPGLE 128

Qy 125 SFPSQAKLRESTPGDSPSTVKNLLQLPSTTTIENISVSVHQPKHIKLAKRRIPPASKIP 184
Db 129 SFPSQAKLRESTPGDSPSTVKNLLQLPSTTTIENISVSVHQPKHIKLAKRRIPPASKIP 188

Qy 185 ASAVEMPGSADVTGLNVQFGALEFGSPSESGFSGAPSSSENSNQIPISLSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGALEFGSPSESGFSGAPSSSENSNQIPISLSKSLSEPLNT 248

Qy 245 SLSMTSAVQNSTYTTTTSVITSCSLTSSSLNSASPVMSSSYDQSSVHNRIPIYQSPVSSSES 304
Db 249 SLSMTSAVQNSTYTTTTSVITSCSLTSSSLNSASPVMSSSYDQSSVHNRIPIYQSPVSSSES 308

Qy 305 APGTIMNGHGGRSQQTLD 324
Db 309 APGTIMNGHGGRSQQTLD 328

RESULT 7
US-10-176-483-252
; Sequence 252, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C68
; CURRENT APPLICATION NUMBER: US/10/176,483
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-483-252

Query Match 37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKXANITSSQILDQKAPSLGQTTTPTSTQON 64
Db 9 NSVLLRICSFPLKSSVLGSGFGLAPPKXANITSSQILDQKAPSLGQTTTPTSTQON 68

Qy 65 STSHPTTTTSDLKPPPTSQSSVLSHLDFKSPSPVLSQSLSQOQHQSOAVTTPPPGLE 124
Db 69 STSHPTTTTSDLKPPPTSQSSVLSHLDFKSPSPVLSQSLSQOQHQSOAVTTPPPGLE 128

Qy 125 SFPSQAKLRESTPGDSPSTVKNLLQLPSTTTIENISVSVHQPKHIKLAKRRIPPASKIP 184

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Db 129 SPFSQAKLRESTPGDSFSTVKNLLQLPSTTIENISVSVHQPOPKHKLAKRRIPPASKIP 188
QY 185 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFSGAPSENSNQIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFSGAPSENSNQIPISLYSKSLSEPLNT 248
QY 245 SLSMTSAVQNSTVTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSES 304
Db 249 SLSMTSAVQNSTVTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSES 308
QY 305 APGTIMNGHGGGRSQOQLDT 324
Db 309 APGTIMNGHGGGRSQOQLDLS 328
RESULT 8
US-10-176-749-252
; Sequence 252, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-252
Query Match 37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;
QY 7 STAVNSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRIGCFIPLKSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQFTTTPSTQON 68
QY 65 STSHPTTTTSDWKLPKPTSSQSVLSHLDFKSPVLSQSRQOQHSQAVTVPPGPLE 124
Db 69 STSHPTTTTSDWKLPKPTSSQSVLSHLDFKSPVLSQSRQOQHSQAVTVPPGPLE 128
QY 125 SPFSQAKLRESTPGDSFSTVKNLLQLPSTTIENISVSVHQPOPKHKLAKRRIPPASKIP 184
Db 129 SPFSQAKLRESTPGDSFSTVKNLLQLPSTTIENISVSVHQPOPKHKLAKRRIPPASKIP 188
QY 185 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFSGAPSENSNQIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFSGAPSENSNQIPISLYSKSLSEPLNT 248
QY 245 SLSMTSAVQNSTVTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSES 304
Db 249 SLSMTSAVQNSTVTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSES 308
QY 305 APGTIMNGHGGGRSQOQLDT 324
Db 309 APGTIMNGHGGGRSQOQLDLS 328

RESULT 9
US-10-176-914-252
; Sequence 252, Application US/10176914
; Publication No. US20030017543A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C83
; CURRENT APPLICATION NUMBER: US/10/176,914
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-914-252
Query Match 37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;
QY 7 STAVNSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRIGCFIPLKSSVLGSGFGLAPPKMANITSSQILDOLKAPSLGQFTTTPSTQON 68
QY 65 STSHPTTTTSDWKLPKPTSSQSVLSHLDFKSPVLSQSRQOQHSQAVTVPPGPLE 124
Db 69 STSHPTTTTSDWKLPKPTSSQSVLSHLDFKSPVLSQSRQOQHSQAVTVPPGPLE 128
QY 125 SPFSQAKLRESTPGDSFSTVKNLLQLPSTTIENISVSVHQPOPKHKLAKRRIPPASKIP 184
Db 129 SPFSQAKLRESTPGDSFSTVKNLLQLPSTTIENISVSVHQPOPKHKLAKRRIPPASKIP 188
QY 185 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFSGAPSENSNQIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFSGAPSENSNQIPISLYSKSLSEPLNT 248
QY 245 SLSMTSAVQNSTVTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSES 304
Db 249 SLSMTSAVQNSTVTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSES 308
QY 305 APGTIMNGHGGGRSQOQLDT 324
Db 309 APGTIMNGHGGGRSQOQLDLS 328
RESULT 10
US-10-176-915-252
; Sequence 252, Application US/10176915
; Publication No. US20030017544A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.

```
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/176,915
; CURRENT FILING DATE: 2002-06-21
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-915-252

Query Match      37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFIPLLKSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 68
Qy 65 STSHPTTTTSDWLKPPTSSQSSVLSHLDFKSPQPEPSPVLSQLSQRQHQSOAVTVPPPGLE 124
Db 69 STSHPTTTTSDWLKPPTSSQSSVLSHLDFKSPQPEPSPVLSQLSQRQHQSOAVTVPPPGLE 128
Qy 125 SFPQAKLRESTPGDSPSTVKNLQLPSTTIENISVSVHQPKHIKAKRIRIPASKIP 184
Db 129 SFPQAKLRESTPGDSPSTVKNLQLPSTTIENISVSVHQPKHIKAKRIRIPASKIP 188
Qy 185 ASAVEMPGSADVTGLNVQFGLERFSGPSLSEFGSAPSSSENSNOIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLERFSGPSLSEFGSAPSSSENSNOIPISLYSKSLSEPLNT 248
Qy 245 SLSMTSAVONSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPTYQSPVSSSES 304
Db 249 SLSMTSAVONSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPTYQSPVSSSES 308
Qy 305 APGTIMNGHGGGRSQOQLDT 324
Db 309 APGTIMNGHGGGRSQOQLDS 328

RESULT 11
US-10-173-706-252
; Sequence 252, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-252

Query Match      37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFIPLLKSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 68
Qy 65 STSHPTTTTSDWLKPPTSSQSSVLSHLDFKSPQPEPSPVLSQLSQRQHQSOAVTVPPPGLE 124
Db 69 STSHPTTTTSDWLKPPTSSQSSVLSHLDFKSPQPEPSPVLSQLSQRQHQSOAVTVPPPGLE 128
Qy 125 SFPQAKLRESTPGDSPSTVKNLQLPSTTIENISVSVHQPKHIKAKRIRIPASKIP 184
Db 129 SFPQAKLRESTPGDSPSTVKNLQLPSTTIENISVSVHQPKHIKAKRIRIPASKIP 188
Qy 185 ASAVEMPGSADVTGLNVQFGLERFSGPSLSEFGSAPSSSENSNOIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGSADVTGLNVQFGLERFSGPSLSEFGSAPSSSENSNOIPISLYSKSLSEPLNT 248
Qy 245 SLSMTSAVONSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPTYQSPVSSSES 304
Db 249 SLSMTSAVONSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPTYQSPVSSSES 308
Qy 305 APGTIMNGHGGGRSQOQLDT 324
Db 309 APGTIMNGHGGGRSQOQLDS 328

RESULT 12
US-10-175-738-252
; Sequence 252, Application US/10175738
; Publication No. US20030022294A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C45
; CURRENT APPLICATION NUMBER: US/10/175,738
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-738-252

Query Match      37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

Qy 7 SSTAVNSCS--PQSLSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 64
Db 9 NSVLLRICSFIPLLKSSVLGSGFGLAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 68
Qy 65 STSHPTTTTSDWLKPPTSSQSSVLSHLDFKSPQPEPSPVLSQLSQRQHQSOAVTVPPPGLE 124
Db 69 STSHPTTTTSDWLKPPTSSQSSVLSHLDFKSPQPEPSPVLSQLSQRQHQSOAVTVPPPGLE 128
Qy 125 SFPQAKLRESTPGDSPSTVKNLQLPSTTIENISVSVHQPKHIKAKRIRIPASKIP 184
Db 129 SFPQAKLRESTPGDSPSTVKNLQLPSTTIENISVSVHQPKHIKAKRIRIPASKIP 188
```

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185 ASAVEMPGSADVTGLNVQFALERGSEPLSEFGSAPSSSENSNQIPISLYSKSLSEP LNT 244
    |||
Db   |||
189 ASAVEMPGSADVTGLNVQFALERGSEPLSEFGSAPSSSENSNQIPISLYSKSLSEP LNT 248
    |||
Qy   |||
245 SLSMTSAVONSTYTTSVITSCSLTSSSLNGASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
    |||
Db   |||
249 SLSMTSAVQNSTYTTSVITSCSLTSSSLNGASPVMSSSYDQSSVHNRIPIQSPVSSSES 308
    |||
Qy   |||
305 APGTMNMGHGGGRSQOQLDT 324
    |||
Db   |||
309 APGTMNMGHGGGRSQOQLDS 328

RESULT 13
US-10-175-752-252
; Sequence 252, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC60
; CURRENT APPLICATION NUMBER: US/10/175,752
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-752-252

Query Match      37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative . 3; Mismatches 7; Indels 2; Gaps 14

Qy   7 SSTAVNSCS--POSLSVLGSFGFELAPPKMANITSSQILDQLKAPSLGQTTFTPSQON 64
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   9 NSVLLRICESFIPLKKSVLGSFGFELAPPKMANITSSQILDQLKAPSLGQTTFTPSQON 68
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy   65 STSHPTTTTSWDLKPTSQSSVLSHLDFKSQPEPVLSQLSOROHQSQA VTVPPGLE 128
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   69 STSHPTTTTSWDLKPTSQSSVLSHLDFKSQPEPVLSQLSORQHQSQA VTVPPGLE 128
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy   125 SFPSQAKLRESTPGDSPSTWNKLLQLPSTTIENISVSVHQPOPKHIKLAKERRIPPASKIP 184
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   129 SFPSQAKLRESTPGDSPSTWNKLLQLPSTTIENISVSVHQPOPKHIKLAKERRIPPASKIP 188
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy   185 ASAVEMPGSADVTGLNVQFALERGFGEPLSEFGSAPSSSENSNQIPISLYSKSLSEP LNT 244
     |||
Db   189 ASAVEMPGSADVTGLNVQFALERGFGEPLSEFGSAPSSSENSNQIPISLYSKSLSEP LNT 248
     |||
Qy   245 SLSMTSAVONSTYTTSVITSCSLTSSSLNGASPVAMSSSYDQSSVHNRIPIQSPVSSSES 304
     |||
Db   249 SLSMTSAVQNSTYTTSVITSCSLTSSSLNGASPVMSSSYDQSSVHNRIPIQSPVSSSES 308
     |||
Qy   305 APGTMNMGHGGGRSQOQLDT 324
     |||
Db   309 APGTMNMGHGGGRSQOQLDS 328

RESULT 14

```

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430RIC86
; CURRENT APPLICATION NUMBER: US/10/176,757
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 252
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-757-252

Query Match 37.9%; Score 1536; DB 14; Length 363;
Best Local Similarity 96.2%; Pred. No. 3.5e-79;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;

QY	7	SSTAVNSCS--PQSLSSVLGSGFGLAPKMANITSSQILDOLKAPSLGQFTTTSTQON	64
DB	9	NSVLRICSFIPLLKSSVLGSGFGLAPKMANITSSQILDOLKAPSLGQFTTTSTQON	68
QY	65	STSHPTTTTSDWKPTTSQSSVLSHLDPKSQPEPSVLSQLSQROHQHQSOAVTVPPGLE	124
DB	69	STSHPTTTTSDWKPTTSQSSVLSHLDPKSQPEPSVLSQLSQROHQHQSOAVTVPPGLE	128
QY	125	SPPQAKLREPTPGDSPSTVKNLQLPSTTIENISVSVHQPOPKHIKAKRRIPPASKIP	184
DB	129	SPPQAKLREPTPGDSPSTVKNLQLPSTTIENISVSVHQPOPKHIKAKRRIPPASKIP	188
QY	185	ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFEFGSAPSENSNQIPISLYSKSLSEPLNT	244
DB	189	ASAVEMPGSADVTGLNVQFGLFEGSEPSLSFEFGSAPSENSNQIPISLYSKSLSEPLNT	248
QY	245	SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPYQSPVSSSES	304
DB	249	SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPYQSPVSSSES	308
QY	305	APGTIMNGHGGGRSQOTLDT	324
DB	309	APGTIMNGHGGGRSQOTLDS	328

Search completed: January 31, 2005, 17:49:12
Job time : 74 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 31, 2005, 17:38:56 ; Search time 22 Seconds
(without alignments)
3437.563 Million cell updates/sec

Title: US-10-509-307-1
Perfect score: 4055
Sequence: 1 MAPGTGSSAVNSCSPQSLSSVLGSGFGEIAPPKVANNITSSQILDQ--LKAP-SLGQFTTT 786

Scoring table: BLOSUM62
Gapop:10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	378.5	9.3	2232	2 T34434	hypothetical prote
2	360	8.9	1367	1 S48478	glucan 1,4-alpha-g
3	323	8.0	1802	2 S89703	HKR1 protein precu
4	321	7.9	528	2 I47141	gastric mucin (clo
5	314.5	7.8	1032	2 T34433	hypothetical prote
6	299.5	7.4	1104	2 S59310	probable membrane
7	291.5	7.2	534	2 T39903	serine-rich protei
8	289.5	7.1	1306	2 S25370	MSB2 protein - yea
9	286.5	7.1	2090	2 S26058	probable transform
10	280	6.9	2271	2 F90073	hypothetical prote
11	277	6.8	786	2 T16509	hypothetical prote
12	276.5	6.8	1630	2 A53577	ascites sialoglyco
13	274.5	6.8	1199	2 A40670	nuclear envelope p
14	274	6.8	1275	2 T33369	hypothetical prote
15	272.5	6.7	4776	2 E95206	cell wall surface
16	272	6.7	1063	2 D86731	hypothetical prote
17	270.5	6.7	2187	2 T30826	nascent polypeptid
18	270	6.7	3507	2 T34513	hypothetical prote
19	268.5	6.6	2715	2 T13049	eyelid - fruit fly
20	267	6.6	535	2 T37544	hypothetical serin
21	262.5	6.5	833	2 S70577	lipoprotein vsc (
22	261.5	6.4	583	2 S67571	hypothetical prote
23	261.5	6.4	1131	2 T41144	hypothetical serin
24	258.5	6.4	1804	2 H96597	hypothetical prote
25	257.5	6.4	1777	2 T34369	hypothetical prote
26	257.5	6.4	1952	2 T48814	hypothetical prote
27	254.5	6.3	3570	2 T45025	mucin MUC5B, trach
28	252.5	6.2	967	2 S66852	hypothetical prote
29	252	6.2	13288	2 T03099	mucin, submaxillar

ALIGNMENTS

RESULT 1

T34434
hypothetical protein K06A9.1a - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T34434
R:Geisel, C.; Gattung, S.
submitted to the EMBL Data Library, December 1996
A:Description: The sequence of C. elegans cosmid K06A9.
A:Reference number: 221525
A:Accession: T34434
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2232 <GEI>
A:Cross-references: UNIPROT:Q81FX6; EMBL:U80846; PIDN:AAC70890.1; GSPDB:GN00028; CESP:K06A9
A:Experimental source: strain Bristol N2; clone K06A9
C:Genetics:
A:Gene: CESP:K06A9.1a
A:Map position: X
A:Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 1088/1; 1367/1; 2039/1; 2049/1; 2075/

Query Match		9.3%	Score 378.5; DB 2; Length 2232;
Best Local Similarity		22.6%	Pred. No. 7.5e-10;
Matches		216; Conservative 103; Mismatches 330; Indels 305; Gaps 33;	
Qy	2	APGTGSSAVNSCSPQSLSSVLGSGFGEIAPPKVANNITSSQILDQ--LKAP-SLGQFTTT	58
Db	886	SPGSPGTTLTSTSPSPSQSLTIGSTGSGTSPG--ISTTSEMTSGSTQTTPGSGSTVTQ	943
Qy	59	PSTQONST-----SHPTTTSDWLKPPTSQSSVLSHLPKSPSPVLSQ	104
Db	944	PSTVSDSTSGSTVTVGSGSPSPSTQNTNPSTSSGSSMSTQTPQSSQSTSPVSS	1003
Qy	105	LSQRQQRQSOAVTV-----PPGLESPSPQAKL-----RESTGDSPTVNKL	147
Db	1004	TSGATSSSGSPGTTLTSTSPSPSSITGSSQSGTSPVSTISQGSTETPGSTGTVTK-	1062
Qy	148	LQLPSTTIEMISV-----SVHQPQPKHKLAKRRIPPAASKIPASAVEM	190
Db	1063	---PSTVSGSGSGSTATMGSTASSTSGSGSTSPNPSPQ-----STSPSTSGATSS	1110
Qy	191	PGADVTGLNVQ-----FGALEFGSEPSLSEFGAPSENSNOIPIS-----	232
Db	1111	PGSGGTTLTSTSPSPSSITGSSQSGTSPVSTTSGDMSQTQIPGSGSTVTPST	1170
Qy	233	-----LYSKSLSEPLNTSLSMTSYAVQNSYV-----	257
Db	1171	SGSGSTSGSITSGSTQTPRSSLTSTPAISTSTQOSVSTNSPGSTVTVQSTVSGTSSG	1230
Qy	258	-----TTSVITSCSLTSSLSNASPV-AMSSYDQSSVHNRIPIYQSPVSSSSAPGTI	309
Db	1231	STVTTGSGSTSGSSSATSLSSSPVPSTSQSPNPSTSGSSTPTPNPSSQSTSPVSTT	1290

Proc. Natl. Acad. Sci. U.S.A. 93, 8419-8424, 1996
A>Title: Muc1, a mucin-like protein that is regulated by Msa10, is critical for pseudohy
A;Reference number: JC6123; MUID:96323237; PMID:8710886
A;Accession: JC6123
A;Status: nucleic acid sequence not shown
A:Molecule type: DNA
A;Residues: 1-1367 <LAM>
A;Cross-references: GB:U30626; NID:gl1304386; PIDN:AAC49609.1; PID:gl1304387
C;Genetics:
A;Gene: SGD:MUC1; STA2; MAL5; DEK2; SGD:S0001458
A;Cross-references: MIPS:YIR019c; SGD:S0001458
A;Map position: 9R
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase 1
C;Keywords: glycosidase; hydrolase; polysaccharide degradation; transmembrane protein
F:5-21/Domain: transmembrane #status predicted <TM1>
F:1350-1366/Domain: transmembrane #status predicted <TM2>

Query Match 8.9%; Score 360; DB 1; Length 1367;
Best Local Similarity 24.7%; Pred. No. 3e-09;
Matches 201; Conservative 103; Mismatches 328; Indels 182; Gaps 34;

QY 2 APTGSGSTAVNSCSFQSLSSVLGSGFCELPKMANITSSQILDQLKAPSLGQFTTPT 61
DB 258 APATPTT---SCTKE-----KTPPTTCTCKE-----PTPHHDITPT 296
QY 62 QONSTSHPTTTSWDLKPTSSQSVLHLDKSPKPEPVLSQLSQ-----RQHQSOA 115
DB 297 KKTTTCTCTKTTTPVTPSSST--TESSAPVTPSSSTTESSAPVTPSSSTESS 353
QY 116 VTPPPGLSPQAKURESTPGSPSTVNVKLLPSTTIENISVSHQPKHKLAKR 175
DB 354 APVTPSSSTTES-----SSAPVTSSTTESAPVTSSTTESAPV--PTPSSSTTES 406
QY 176 RPPAKIPASAVEMPGSADVTGLNVQFALFEGSEP---SLSEFGSAP---SSENNQI 229
DB 407 SAPVTSSTTES-----SAPVTS-----STTESAPVTSSTTESAPVTSSTTES 456
QY 230 PISLYSKLSLSE---PLNTSLSMSTA--VQNSTVTTSTVITSCSLTSSLSNAS--PVAM 280
DB 457 PVPPTSSSTTESAPVTSSTTESAPVTPSSSTTESAPVTPSSSTTESAPVTPSS 516
QY 281 SSSYQSSVHNRIPQSPVSS---SESAPGTIMHGCGRQQTLDTPKTKTPPSALPSV 337
DB 517 SSTTESA-----PAPTSSSTTESAPVTP-----SSTTESAPVTP--PSSSTTES 564
QY 338 SSLPSTTCTCT---ALLPSTSQHTGDLTSSPLSQLSSLSHQSLSHAAALSSSTSTH 393
DB 565 STPTVTSSTTESAPVTPSSSTTESAPVTPSSS--TTESAPAPTPSSSTTES 623
QY 394 ASVESASHQSSATFTSTAATSVSSASGCVLSSSMNTANSICLGTTPASASSSSRA-- 451
DB 624 APVTSSTTESAPVTPSSSTTESAPVTPSSSTTESAPVTPSSSTTESAPVTPSS 683
QY 452 -----APLVTSKAPNLPQGVPPPLHNNQYLVGQGLLPAYPIYGVDELMQLQSL 502
DB 684 TSSTTESAPVTSSTTESAPVTPSSSTTESAPVTPSSSTTESAPVTPSSSTTES 739
QY 503 PVDYIGIPFAAPTALASDRSLANNYPGDVTKFGRGDSASAPATTPAQ----- 552
DB 740 PSSSTTESAPVTSSTTESAPVTPSSST-----TESSAPVTPSSSTTESAPV 794
QY 553 PQOSQTHHTAQPFVNALPGYGV-----TGLPYVTGMPSAFOGPTMFVPPASA 605
DB 795 PTPSSSTTES-----VAPVTPSSSNITSNAPSTPSSSTTESVVPVTPSSSTTES 849
QY 606 KQGVNLST-----PTP-----PFQASGVGHGYSYGYDDLTQGTAA 643
DB 850 SSAPVSSSTTESVAVPVTPTSSSNITSGAPSSIPFSSTT---ESFST----- 894
QY 644 GDYSKGGYAGSSOAPNKSAGSGPKGVSVSSSTTGLPDMTGSVYNTQTQFQKGFHAGT 703
DB 895 -----GTTVTPSSSKYPGSGTSTSTESSTT-----TTIVPTKTTT-----SVTTP 934

QY 310 ---MNGHGGGRSQOTLDT---PKT-----TGPP--SAL 334
DB 1291 TGMWTHGGSTQTPSTIGSTVTPQSTVSGNSGSGTWTIGSSEASTSGSFKTSPPSISPV 1350
QY 335 PVSLSLPSTT-----SCTALLP-----STSQHTGDLT 361
DB 1351 PTSPPPTPTFASTSGSTISDVSVSTTSLAPLSSLPSTVPSSSTQFSSTSESSKAS 1410
QY 362 SSPL--SOLSSS---LSSHQSSLSAAALSSSTSHTHASVESASHQSSATESTAA--SV 415
DB 1411 SSPVPSSTSTPTNPTGSESTLLSSTIGSTQHTTMEKASGSGSTSPSTNSQSTGVTM 1470
QY 416 SSNASSGVLSSSMNTANSICLGTTPASASSSSSRAAPLVTSKAPPNLPQGVPPLLHNO 475
DB 1471 GSSSTSGVSTSSAST-----QPMSTSQSSAGSTVASSTASPAASSTAPSSTGTM 1522
QY 476 YLVGPGGLLPAYPIYGYDELMQLQSLRPVDYIGIPFAAPTALASDRSLANNYPGDVTK 535
DB 1523 SSTSSGTV-----GSTISESTTASASQSTGSTVTM 1553
QY 536 FGRGDSAPAPATPAPOQSOQ-----THHTAQPFVNALPGYGVTLGPPYVTGMP 589
DB 1554 GSSSTSGVSTSSASTQPMSTSQSSAGSTVASTAGLVSTVP--SSTGT---MSGT 1608
QY 590 SAFQYGTPTFPPASAKQGVNLSTPTPPFQQAAGYGHGYSYGYDDLT---TQGTAAGD-- 645
DB 1609 SSGTVGSTITSESTTASASQSTGVTVMGSSSTSGVSTSSASTQPMSTSQSSAGSTV 1668
QY 646 -----YSKGVYAGSSOAPNKS-----GSGPKGYVS 671
DB 1669 ASSTTGLVSTVTPSSTGTMGSSSTSGVSTSSSTTASASQSTGVTVMGSSSTSGVS 1728
QY 672 VSSSTGLPDMTGSVYNTQTFDQGFHAGTTPPPFSLPSVLGST--GPLASGAP 724
DB 1729 TSSASSGQPMST-----QGSAGS-----TVVSTASPAASSTAP 1765

RESULT 2
S48478
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - yeast (Saccharomyces cerevisiae)
N;Alternate names: extracellular glucoamylase; mucin-like protein MUC1; protein YIR019c
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S48478; B26877; S27281; JC6123
R;Rowley, K.
submitted to the EMBL Data Library, October 1994
A;Reference number: S48478
A;Accession: S48478
A:Molecule type: DNA
A;Residues: 1-1367 <ROW>
A;Cross-references: UNIPROT:P08640; GB:Z47047; EMBL:Z38061; NID:g603997; PID:g763364; GS
R;Yamashita, I.; Nakamura, M.; Fukui, S.
J. Bacteriol. 169, 2142-2149, 1987
A;Title: Gene fusion is a possible mechanism underlying the evolution of STAL.
A;Reference number: A91831; MUID:87194600; PMID:3106330
A;Accession: A26877
A:Molecule type: DNA
A;Residues: 1-242 <YAM>
A;Cross-references: EMBL:M16164; NID:g172522; PIDN:AAA35014.1; PID:g172525
A;Accession: B26877
A:Molecule type: DNA
A;Residues: 762-1331 <YA2>
A;Cross-references: EMBL:M16165; NID:g172523; PIDN:AAA35015.1; PID:g172526
R;Pardo, J.M.; Ianez, E.; Zalacain, M.; Claros, M.G.; Jimenez, A.
FEBS Lett. 239, 179-184, 1988
A;Title: Similar short elements in the 5' regions of the STA2 and SGA genes from Sacchar
A;Reference number: S27281; MUID:89031230; PMID:3141213
A;Accession: S27281
A:Molecule type: DNA
A;Residues: 1-31 <PAR>
A;Cross-references: EMBL:X13857; NID:g4551; PIDN:CAA32069.1; PID:g4552
R;Lambrechts, M.G.; Bauer, F.F.; Marmur, J.; Pretorius, I.S.

Query Match	8.0%;	Score 323;	DB 2;	Length 1802;									
Best Local Similarity	23.0%;	Pred. No. 2.le-07;											
Matches	208;	Conservative 124;	Mismatches 361;	Indels 210;	Gaps 38;								
Qy	5	TGS	TAVN	SCPSQ	SSVLSS	VGFGEL	APPK	MANITSSOIL	DOLK	APSLGQ	TTTTSTP	STQON	64
Db	50	TG	SNKEN	AVNTSS	SETT	MACQ	YEGS	-----	ST	IMDE	QFTG	SSQIS	101
Qy	65	STSH	TTTT	TSW	LK	PPTS	QSSV	LGH	LP	KSP	QPP	SPVL	119
Db	102	SDT	MSSV	KK	ST	EI	ATPS	--SSIV	-----	PT	PQ	SYD	149
Qy	120	PP	GLES	PP	SO	A	K	RES	PGDS	--P	STV	NK	170
Db	150	DS	DTT	SS	SS	SV	I	STD	S	AV	P	RE	205
Qy	171	KL	KRR	1	P	P	A	S	A	V	E	M	226
Db	206	AQ	M	TR	V	S	Q	I	S	S	I	A	249
Qy	227	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	257
Db	250	Y	M	S	K	S	Q	L	S	E	S	S	309
Qy	258	T	T	V	I	T	S	C	L	S	S	S	313
Db	310	R	P	S	S	I	T	--Q	T	S	I	D	365
Qy	314	G	G	R	S	Q	O	L	T	P	K	T	360
Db	366	G	V	S	R	E	S	N	T	F	V	S	425
Qy	361	T	S	S	P	L	S	Q	L	S	S	L	409

DEPOSIT A

QY	125	SPPSOAKLRETPGSPSTVNNKLLQLPSTTINISVSHQPOPKHKLAKRRIPASKIP	184
Db	102	SSSSSAPISSTTSVQPSSSG--SVPTTSATSVQSSSSSAP-----TTSATSVQ	150
QY	185	ASAVENPGADVTGLNVQGALEFGSEPSLSFEGSAPSENNOQIPISLYSKLSEPLNT	244
Db	151	SSSSSPPISSTVS-----VQPSSS--SSAPTTSATSVQ-----SSSSSPPIS	192
QY	245	SLSMTSAVONSTVTTTSVITSSCLTSSLSNSAPVAMSSSYDQSSVHNRIYQSPV--SSS	302
Db	193	TVSVQVTSSSSVTTTTSVQPSSSSVPTTSATSVRS--SSSTPIPTTSVQPSSS	249
QY	303	ESAPGTMMHGGGRGSOQLDTPKTTGPPSALPVSLSLSTTSCTALLPSTSQHGTDLTS	362
Db	250	SSAPTTSATSVQPSSSST-PIPTTT--SVQPSSSSAPTTSATSVQPSSS-----S	298
QY	363	SPLSOLSSLSHQSSLSAHAALLSSTSHTHASVESASHQGSATPSTTAATSVSSASG	422
Db	299	SP--PISSTISVQPSSS--SSPTTST-TSVQPSSSGSAP--TTSATSVQPSSSS	347
QY	423	VSLSSNMNTANSLCLGCTPASASSSSRAAPLV---TSGKAPPNLPQGVPPPLHNOYLVG	479
Db	348	PIISSITSV-----QPSSSSSPTTSTTSVQPSSSGAPTTSATSVQPSSS-----	394
QY	480	PGLLPAPYIYGYDELQMLQSLRPVDYIGIPFAAPTALASDRSLANNYPGDTVKEGRG	539
Db	395	-----SVPTTSATSVRSSS-----	409
QY	540	DSASPAPATTAPQOQSOTHTTAQPFVNPALPGYSYGLPYTGMPSAFQYPTMF	599
Db	410	-SSTPIPTTSVQPSSSS-----	427
QY	600	VPASAK--QGVNLSSTPTFPQAGSYGQGYSTGYNDLTQGTAAQDYKSGYAGSSQA	657
Db	428	VPTTSATSVQTSSSSTPIPTTSVQ-----SSSSSA	460
QY	658	PNKAGSGPGKGVSVSSSTGLPDMTGSVYNTQTDPKQGFHAGTTPPFSLPSVLASTGP	717
Db	461	PTTSA-----TSVQPSSSSSPISSTI-----SVQP	486
QY	718	LASGAAPGYAPPPPLHLPAAHQPHSOLLHHLPQAQSGSGQSORSPSSLPKQSKAP	776
Db	487	SSSSSPTTTSV-----QPSSSGSAPTTSATSVQPSSSSPP	525
RESULT 5			
T34433			
hypothetical protein K06A9.1a - Caenorhabditis elegans			
C/Species: Caenorhabditis elegans			
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004			
C/Accession: T34433			
R/Geisel, C.; Gattung, S.			
submitted to the EMBL Data Library, December 1996			
A/Description: The sequence of C. elegans cosmid K06A9.			
A/Reference number: 221525			
A/Accession: T34433			
A/Status: preliminary; translated from GB/EMBL/DBJ			
A/Molecule type: DNA			
A/Residues: 1-1032 <GEI>			
A/Cross-references: UNIPROT:P91365; EMBL:U08046; PIDN:AACT0889.1; GSPDB:GN00028; CESP:K06A9			
A/Experimental source: strain Bristol N2; clone K06A9			
C/Genetics:			
A/Gene: CESP:K06A9.1a			
A/Map position: X			
A/Introns: 38/1; 75/3; 103/3; 132/2; 158/2; 222/1; 839/1; 849/1; 875/3; 940/2; 966/2; 99			
Query Match			
Best Local Similarity 7.8%; Score 314.5; DB 2; Length 1032;			
Matches 195; Conservative 98; Mismatches 284; Indels 199; Gaps 35;			
QY	5	TGSSTAVNSCSFQSL---SSVLGSGFGLAPPKVANTTSOILDLQKAPSLGQTTTPTST	61

Db	224	TSPSTAVT--SPSILGTSSSPLPSSISITSALPIASSASS--SPSAAS-STTPVW	273
QY	62	QONSTSHPTTTTNDLKPPTQSQSVLSHLDPKSPSPVLSQSQORQHQSOAVTVPVP	121
Db	274	LSSSTIOSSSGTF-----PSSVASSPSTVGTSTGAASSSVATVSTIAGTGTIT-PVP	327
QY	122	GLESPFOAKLRESTPGDPSPTVNNKLQLPSTTTIENISVSHVQPPQKHKLAKRRIPP--	179
Db	328	G-----SSSTIGSTTPSASSSSSGTMTISGSGSTTV-----VPGSS	366
QY	180	---ASKIPASAVEMPGSADVT---GLNVQFALFEGSEPSLSEFGSAPSSNSNQ-----	228
Db	367	STFASSTPIASSSSPGST-VTVAPGSSSTYGS-----STPSASSSSSGTMTNSGSGT	421
QY	229	--IPISLYSKLSPLNTLSMTSAV-----QNSTYTTTSVITSCSLTSSLSNSASPVAMS	281
Db	422	TVAPVSSSTFGSGSTPIASSSSSGSTTVVSGSSSTYGS---TPSASSSSAGTASTISGS	478
QY	282	SSY-----DOSSVHNRIYQSPVSSSESAPGTMMHGGGRGSOQLDTPKTTGP-PSA	333
Db	479	TCSTATIVPGSSSVGS-----STQASAPSPSGTMTVSGTGTTVVPGSSTSPAPSS	533
QY	334	LPSVSSLSSTTSCTALLPSTSQHGTDLTSPLSQLSSLSHOSLSAHAALSSSTSHTH	393
Db	534	SNPSSSPASTGTITISGSSIIIVSTVSG--STVSGTSGTSGTSLASTATPGSS--	588
QY	394	ASVESASSHQGSATPSTAAAT--SVSSSASSGVSLSSNMNTANSLCLGCTPASASSSSRAA	452
Db	589	-TVPSSSPQPSQSPAPNTVGTSTTSPQTSQSPFSMNPSSS-----TPTGSSQST---	638
QY	453	PLVTSKAPPNLPQGVPPPLHNNQYLVPGLLPAYPIYGYDELQMLQSLRPVDYIGIPFA	512
Db	639	--IT-----PEG-----STASSPTGSGTSTFS	658
QY	513	APTALASDRSLANNYPGDTVTKFGRGDSASAPATTAPQOQSOSQTHHTAQPFVNPA	572
Db	659	VATEVTSQ-----STVPSSSLGTQSTNSSPSPS-----S	688
QY	573	LPPGVSYTGLPYTGMPSAFQYPTMFVPPASAKOHGV--NLSTPTP-PFOQAGYGOHG	629
Db	689	LSP--STGMSLTITSEPS-----PSSTQSSGAQSTLTTPSPNPQSSTSSLESST	735
QY	630	YSTGVDDLTOGTAAQDYKSGYAGSSQ---ANKAGSG-----PGKGVSVSSST	676
Db	736	SGATTSSGAGTMTSPSQSSSVSGSTSPAASTTGEMTSGQSTOTPGSSVSTSAAI	795
QY	677	TGLPDMTGSVYNTQTFDKGFHAGTTPPFSLPSVLGSGTGLASGA--APGYAPPP	730
Db	796	LTSQOQSVSTNSPGSTVTRPSTVSGSTSGSTTVV-GSTEASTSGSLATTSAKP	850
RESULT 6			
S59310			
probable membrane protein YMR317w - yeast (Saccharomyces cerevisiae)			
N/Alternate names: hypothetical protein YMR924.09			
C/Species: Saccharomyces cerevisiae			
C/Date: 29-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 19-Apr-2002			
C/Accession: S59310			
R/Churcher, C.M.			
submitted to the EMBL Data Library, September 1995			
A/Reference number: S59302			
A/Accession: S59310			
A/Molecule type: DNA			
A/Residues: 1-1104 <CHU>			
A/Cross-references: EMBL:Z54141; GSPDB:GN00013; MIPS:YMR317w			
A/Experimental source: strain AB972			
C/Genetics:			
A/Gene: MIPS:YMR317w			
A/Cross-references: SGD:S0004936			
A/Map position: 13R			
Query Match			
Best Local Similarity 7.4%; Score 299.5; DB 2; Length 1104;			
Matches 22.8%; Pred. No. 1.4e-06;			

Matches 205; Conservative 126; Mismatches 342; Indels 225; Gaps 34;

QY 4 QTGS--STAVNSCSPQSLSVLGSGFGLAPPKMANIT-----SQILDQLKAPSLGOFT 56
Db 210 GTTSDASKEVFSSTSDVSLLSS---TSSPASSTISETLPFSSTILSITSPPSVSEAP 265

QY 57 TTPSQQNSTGHPTTTTWDLKPPTPSQSSVLHLDFKQPSPVPVLSQLSORQHOSQAV 116
Db 266 SATSSSVSEASSSTSSSVSEAPLATSSVVSS---EAPSSTSSVSEASPSTSSSVSS 322

QY 117 TVPPPGLSFPSOAKLRSTPGDSPSTVKLLQLPSTTIENISVSHQQPKHKIKLKR 176
Db 323 EISSTTSVSEAPLATSSVVSS-----EAPSSTSSSVSEA----- 360

QY 177 IPPASKIPASAVEMPGSADVTCLNMQFGALFGBGPESLSEFGSAPSSSNQIP----ISL 233
Db 361 --PGSTSSSVSEAPSS--TSSSVSESIESTKSVMMSVESSTATSSLVASSEAPSAISSL 415

QY 234 YKSLSELPLNTSLMWSAQNSTYTTSVITSCSLTSSSLNGASPVAMSSSYDQSSVNRI 299
Db 416 ASSRLFFSKNTSVT-----STLVATEASSVTSLRPSSETLASNIIESLSLT- 463

QY 294 PYQSPVSSSEAGPTIMNHGGGRSQOFLDTPKTKTGPPSALPYSSLSLPTCTALLPST 353
Db 464 GYNSTVITTTAAASTLT-GSKVSSNSNRMATSKTSTSDDLKSKSVIFGNSTVTTGPSA 522

QY 354 SQHTGDLTSSPLSQLSSSL-SHHOSSLSAHAALSSTSSHTHASVEAS-----S 401
Db 523 SI---SLTASPLPSVWMDITSEASSISLNLAASSAPSDNNSTIASASLIIVKTKNVSV 579

QY 402 HQSATFTSTAATSVSSSAGSVLSG-----SMNTANSLCIGGT PASAGSSSSRAAPLV 455
Db 580 SIVSSISTSETTNESNLATSSTLLSNKATARSLSTSNATSGNVPTGTFSSMSHSTSVI 639

QY 456 TSGKAPPNLPQGVPELLHNQYLVGCGLLPAYPIGYDELO-----MLQSRLPVDYYG 508
Db 640 TPGFSTSSAIAINSTVVSSLAG-----YSFSTPESSPTTLTVTSEAPTSSV 689

QY 509 IPFAAP-----TALARDRSLANNPY-PGDVTKRGKGDSAPAPATTPAQ 552
Db 690 MTTSAPPFNNTSARPSPSTASFITESSTSISSVPLASGDTV-----SSLAHNLTTFSA 744

QY 553 PQQSQSO---THHTAQPFVNPALP-PGYSYVTGLPYVTGMPSAFQYQFTMPVPP----- 602
Db 745 PSTSAQIVSKSTTSSSILVTPRIDRCSNGSTASRIATSLPN-----KITFVSLSS TSA 799

QY 603 -----ASAKQ-----HGYNLSPTTPPF-----QAASGYQG 627
Db 800 HARINFTSVLTATAKIETLTSTVNCNPTNYMITKVIVSRRETAIGTVTSCGGCTK 859

QY 628 HGYSTGYDDLQTQ-----GTAAGDYSKGYAGSQAQPN-KSAGSGPGQKV 670
Db 860 NRKETILLITIIDAISTVTTCPEKEVSTTSGEDAE-HTTSTKLINFESTTSESFKDM 917

QY 671 SVSSTTGLPDMTGSVYNKIQTFDKQGFHACTPP-----PFLSPSLVLSGTG--PLASGA 723
Db 918 KTSQETTKAKPGSETVRSSSFVEK-----TSPTRKASPTSFSESAAGNTSVATNAS 971

QY 724 PCYAPPFLHLPLAHQPHSOLLHHUHPDAQSSGGORSQSSLOPQSQAKSPAYGNS 781
Db 972 PSTSP-----SESQGTGSTVEGA---KSKTKNSEGVS 1002

RESULT 7
T39903
serine-rich protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: t39903
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
submitted to the EMBL Data Library, November 1998
A:Reference number: Z21889
A:Accession: t39903

A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-534 <>
A:Cross-references: UNIPROT:O94317; EMBL:AL033534; PIDN:CAA22127.1; GSPDB:GN00067; SPDB:
A:Experimental source: strain 972h-, cosmid c215
C:Genetics:
A:Gene: SPDB:SPBC215.13
A:Map position: 2
C:Superfamily: pig submaxillary mucin

Query Match 7.2%; Score 291.5; DB 2; Length 534;
Best Local Similarity 28.3%; Pred.No.1.e-06;
Matches 134; Conservative 66; Mismatches 172; Indels 101; Gaps 17;

QY		6	GSTAVNSCSPOSTSLSSVLGGFGLAPPKMANITTSQILDQLKAPSLGQFTTPTSQ--	63
Dd	:	:	: :	:
Dd	68	GPTYVGYATPTSSE-	-PSIFESATPSETNSVPVSYY-----SDPATSQLP	115
QY		64	NSTSHTTTNDLKPEPTQSQSVLSHLDFKSQPESPVLSQLSORQHQAQTTPPPGL	123
Dd	:	:	: :	:
Dd	116	SSTSFPSTSS-EYTPTSSTESSLL-----DPSSV-----SSAILPSTSV	155	
QY		124	BSPFOAKLRSTPGDSPVTNKLLQLPSTTIENISVHVHPQPKHIKLAKERIPPASKI	183
Dd	:	:	: :	:
Dd	136	EVISISSLSUSDp-----LTSTFSLSLSTSSSQSFVSSTSTSTFAAPT	203	
QY		184	PASAVEMPAGSADTVTLNVGFALFESEPILSRFGSGAPSSE-NGNQIPISLYSKLSEPL	242
Dd	:	:	: :	:
Dd	204	STSSLSSVVSSVSS-----SSPSSSSSTILTSSLSSTSIISTSSSSS----	248	
QY		243	NTSLMTSAVNQSYTYTVTITSCLTSSSNLNASPAMVGSSDYDQSSVHNRI-P-YQSPVS	300
Dd	:	:	: :	:
Dd	249	STSSLSSSSSSTAASSSSSSIISSSSSSSPTSTSTSISSSSSSSPTSTSTSiS	308	
QY		301	SSESAPGITMN-----CHGGGRSQOTLDTPKTGPSPALPVSSLPSTTS---CTALL	350
Dd	:	:	: :	:
Dd	309	SSSSSSSPSTSLSSSMSSSSFFSSPTSSSTTSSSSSPSSSSFSTTSSKKSSSF	368	
QY		351	PSTSHGTDLTGSPISOLSS-----SLSSHQSLSAHAALSSTSHTHASVESASHOS	404
Dd	:	:	: :	:
Dd	369	STTVSSSSSTSSSTLTSSSSRRPASSSHSSLSHSKHSSSS-----KSSAPVS	420	
QY		405	SATFTATAIVSSASSGVSLSSMMTNANSLCGTTPASASSSSRAAPLVTS	457
Dd	:	:	: :	:
Dd	421	SAFYHNSTSRSSHHSHSLSS-----LSCKPIALTASSSS----LLTS	460	

RESULT 8
S25370
MSB2 protein - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein G4017; protein YGR014w
C:Species: Saccharomyces cerevisiae
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: S25370; S64305
R:Bender, A.; Pringle, J.R.
Yeast 8, 315-323, 1992
A>Title: A Ser/Thr-rich multicopy suppressor of acdc24 bud emergence defect.
A:Reference number: S25370; PMID:92383951; PMID:1514328
A:Accession: S25370
A:Molecule type: DNA
A:Residues: 1-1306 <BN>
A:Cross-references: UNIPROT:P32334; GB:M77354; NID:g171993; PIDN:AAA34798.1; PID:g171994
R:Rieger, M.; Mueller-Auer, S.; Brueckner, M.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64071
A:Accession: S64305
A:Molecule type: DNA
A:Residues: 1-1306 <RIE>
A:Cross-references: EMBL:Z72799; NID:g1322977; PID:g1322978; MIPS:YGR014w
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:MSB2
A:Cross-references: SGD:S0003246; MIPS:YGR014w

A:Map position: 7R
C:Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
C:Accession: S26058
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Keywords: transmembrane protein
F:3-19/Domain: transmembrane #status predicted <TM1>
F:1189-1205/Domain: transmembrane #status predicted <TM2>

Query Match 7.1%; Score 289.5; DB 2; Length 1306;
Best Local Similarity 24.0%; Pred. No. 5e-06;
Matches 211; Conservative 110; Mismatches 365; Indels 193; Gaps 39;

QY	2	APGCGSTAVNSCPQSLGSGFGEAPKMANIT---SSQILDQ-----LKAPSL	52
DB	180	APLTSTPLISTMSAADNVFS-----ANPISASLTITDSESPDQSTAGAPVQSS	234
QY	53	GQFTTT-----PSTQONSTSHPTTT--TSNDLKP-PTSQSS-----VLSHLDKFSQ	95
DB	235	ADFSSESILVQSADFPSPFTTIDISLSAAPLOTSESSSPTTASAAALPVSTDDVGS	294
QY	96	PEPSPVLSQLSQRQHQSOQAVTVPPGLESFPQAKLRSTGDSPTVKNKLLQLP--ST	153
DB	295	-SASPVS-MSAAGQIASSSSDTNPMTSETFLTS--TEVDGSDVSTVSALLSAPFLQT	350
QY	154	TIENISVHQPKHIKLAKRIPPASKIPA-SAVEMPGSADVTGLNVQFGAL-----E	207
DB	351	STSN-SFSIVSPS-----VSFVPSQSSDVASSSTANVVSFSFDIPQGTST	396
QY	208	FGGEPSPLEFGSAPFSSNSNQIPISYKSLSEPLNTSLGMSAVQNSVTYTSVITSCSL	267
DB	397	SGSVVVAQASALAFQSGSTEV---YGASASSTMSLLSTTS-LOSTLTDSSSLASSA	451
QY	268	TSSSL-----NSASPVMSSSYDQSVVHNRIPYQSPVSS-----SESAPTGMN	311
DB	452	SSDLTDYGVSTASIPLLSASEQATSSSFVSFVPSQSSDVASTGAPSVSS	511
QY	312	G-----HGGERSQQLDTPKTTGPPALPSVSLPSTTCTALLPSTSGHDLTSSPL	365
DB	512	SFVTSIQAGSSMNPSSSTIVYSSSTGSEESAATASATLGGSSSTVMAGNLQSQPP	571
QY	366	SQLSSSLSSHQSLSAHAALSSSTSHT-----HASVE-----SASHQSSNATFS	409
DB	572	S--TSSLSESQATSTSAVLASSSVSTSPYTTAGGASTASSLSISTSAETQSVYSQS	629
QY	410	TAATSVSSSSSGV---SLSSSMNTANSLCLGGTPASASSSSRAAPLVTSGKAPNLPQ	466
DB	630	TTALQTSFASSTTEGETSSQGFSTSSVLVQMPSSISSEFPSPQTTQWNSASSS---	686
QY	467	GVPPILLNQYLVGPGLLP-----AYPIYGYDELMQSRLLPVDYIGIPFAAPTALAS	519
DB	687	-----SQYTISSGTILLSQVSDTSVSYTTSSSSVSQV--SDTPVSY-----TTSSS	729
QY	520	RDRSLANNPYPGDVTKFGRGDSAPAPATTAPAQOQSQSTHHTAQOQFVNPALPPGYSY	579
DB	730	SVSQVSDTP-----VSYTTSSSSVSQVSDTPVSYTTSSSSVSQVSDTP-----	772
QY	580	TCLPYTGMPSAFQYGPMTFVPASAKQGVNLS--TPTPPQQAAGYGCQHGYSYGYDDL	638
DB	773	--VSYTTSSSSVSQVSDTS--VPSTSSRSVSQVSDTPVSTSSRSVSQ--TSSSLQPT	827
QY	639	QCTAAGDYSKGYAGSQAPNKSAGSGPKGVSVSSSTTGLPDMTGVSYNKTQTFDKQGF	698
DB	828	TSSQRTIITHGALSESSVSQA-----SEITSSINATASEYHSIQ-----	870
QY	699	HAGTPPPPSLPSVLGSGTGLASGAPGYAPPPFLHILPAHQPHSQLL-----HHHL	754
DB	871	TAATQ-----STLSFTDANSSAS---APLEVATSTTPPSKASLLLTFTSSLSQVA	922
QY	755	QSGSGQRS-----OPSSILQPKSQASKPAYGNPSYW	784
DB	923	TWNVQTSLTSTSTTVLEPSTTNSSTTSLVTSDDNNW	961

Db 1690 TGSTASTAAT---PQVSSS-----GF---SSPARGTTAPGVFGQTTTGGQASVF 1732
Qy 716 GPLASGAAP--GYAPPPPLHILPAHQPHSOLLHHHLFPDQAQSGS--GQRQPSLSLOPKS 771
Db 1733 GQSASSAASVFSQPGFSSV-PAFGQPASS-----TPTTSGSVFGAASSTSSSSFS 1785
Qy 772 -----QASKPAYGNP 782
Db 1786 FGQSPNTGGGLFGQSNAPAFQSP 1810

RESULT 10
F90073
hypothetical protein SA2447 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F90073
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:213111952; PMID:11418146
A:Accession: F90073
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2271 <KUR>
A:Cross-references: UNIPROT:Q990Y4; GB:BA000018; PID:g13702612; PIDN:BA843752.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA2447

Query Match 6.9%; Score 280; DB 2; Length 2271;
Best Local Similarity 22.3%; Pred. No. 2.6e-05;
Matches 166; Conservative 106; Mismatches 289; Indels 184; Gaps 23;

Qy 8 STAVNSCPQSLSSVLGSGFE-LAPPKMANITISQILDQKAPSLQOFTTTPSTQNST 66
Db 1088 STSGMSASQDSMSISFSDSTSDSKASASTASGESISQASSTSGSVSTSLSTSN 1147
Qy 67 SHPTTTTSD-----LKPTQSSVLSHLDFKQEPSPVLSQSORQHQSOA 115
Db 1148 SERTSTSVSDSTSLSTSESISSTSDSISEA--ISASESTISISLSEGNSTSDSESQS 1206
Qy 116 VTVPPEGLSEPPSOAKLRESPGSPSTVKNLQLPSTTIENISVHQPOPKHKLAKR 175
Db 1207 AS-----AFLSES-LSESTSESTSESVS-----SSTSESTSL----- 1238
Qy 176 RIPPASKIPASAVEMPGSADVTGLNVQFALFEGFSEPSLSFEGSAPSEN-SNOIPISL- 233
Db 1239 -----DSTSESGSTSLSTSGSASISGTSTISBSTSTFKSESVSTSLSMST 1288
Qy 234 YKSLSEPLNTSL-MTSVAVONSTYTTSTVITSCILTSLSLNAS-PVAMSSSYDQSSVHN 291
Db 1289 TSLSNSTSLSTSLSDSTSDSKSLSTSMSTSDISSTKSDISSTSLSGSTSESE--- 1345
Qy 292 RIYQSPVSSSEAPGTIMNGHGGRSQOQLDTPKTPGPPALPSVSLPSTCTALLP 351
Db 1346 -----SDTSSSEK-----SDTSMISMSQSTSGSTST 1377
Qy 352 STQHTGDLTSPSLQSLSSLSHQSLSAHAALSSSTSHTHASVEGASHQSSATFSTA 411
Db 1378 -STS-----LSDSTSLSLASMMQSGVDSNASQASASNSTSTST-SESDSQSTSTVSQ 1431
Qy 412 ATSVSSGASSGVLSSSMNTANSICLGG---TPASASSSSRAAPLVTSKAPNLPQGV 468
Db 1432 STQSESTSTSLSTSLSTSKSTSQSGSTSTSLSGSESESDSISSTASESTESA 1491
Qy 469 PPLHNYLVGPGGLLPAYPIYGVDELQMLQSLRPVDYIGIPPAAPTALASRDRSLANNP 528
Db 1492 STLSLSDSTSTNSG-----SASTSTSLSNS- 1516
Qy 529 YPGDVTFRGDSASAPA-TTPAQPOQSQTHTTAQQPFVNPAALPGYSYTLGYTGT 587

Db 1517 -----ASASESDSSSTSLSDSTSTASMQSESSEDSTSA----- 1549
Qy 588 MPSAFQYPTMFVPPASAKHQGVNLSTPTTFFQQAAGVGHGYSTGVYDGLTQGTAAAGDYS 647
Db 1550 -----SLSDLSLSTSTNRMSTIASLSTSV-----STSESGSTSESTSDSTSTSLSDSQS 1600
Qy 648 KGGYAGSSQAPNKSAGPGKGVSVSSSTTGLPDMTGVNVNKTQTFKQKQPHAGTTPPPFS 707
Db 1601 TSTRSTSASGASSTSTSTSDSRSTASSTST-----MRTSTSDSQSNLSLSTSTST 1650
Qy 708 L-----PSVLGSGTGLGAAAPG 725
Db 1651 MSDSTSLSDSVSDSTSDSTASTSG 1675

RESULT 11
T16509
hypothetical protein F59A6.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16509
R:Nhan, M.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid F59A6.
A:Reference number: Z18526
A:Accession: T16509
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-786 <NHA>
A:Cross-references: UNIPROT:Q21027; EMBL:U41994; NID:g1123047; PID:g1123052; PIDN:AAA834
C:Genetics:
A:Gene: CESP:F59A6.3
A:Introns: 106/1; 620/1; 634/3; 675/3; 775/1

Query Match 6.8%; Score 277; DB 2; Length 786;
Best Local Similarity 22.1%; Pred. No. 1e-05;
Matches 174; Conservative 90; Mismatches 299; Indels 226; Gaps 29;

Qy 51 SLGQFTTTPSTQONS-----TSHTTTTSDWLKPPTSQSSVLSHLD-----FKSQ-- 95
Db 17 ALSESSTPSTSLSCVWLGDGFATDKTNEYKGTCTSEAVELENESEKWLKSEET 76
Qy 96 -----PEPSPVLSQSORQHQSOAVTPPPGLESPFSQAALRESTP 137
Db 77 TERWNGLTQFLFCVKGACSDPSPWNTCTTSTASTFTI-----SSTSLKST- 126
Qy 138 GDSPSTVKNLQLPSTTIENISVHQPOPKHKLAKRIPPASKIPASAVEMPGSADVT 197
Db 127 SDSTSTEPRI-----STTDTKDTTTEDPVS---STDQSSTSPHETTRDTTTEGTTSEDT 179
Qy 198 GLNVQFALFEGSEPS-LSEFGSAPSE-----NSNQIPISLKYKSLSEPL-----NT 244
Db 180 S-----TYGSTRSSPKPTSEFTSTEDFTSTRSTSTSIETNSSTSPVSTTPEYDST 236
Qy 245 SLGNTSAVQNSTYTTSTVITS-----CSLTSSLSNASAPV-----A 279
Db 237 SSGNSETTSDGTTTTFVTTKDDTSTVSGDSNNGSSTSEFQNTETTTGPGSTVSEPS 296
Qy 280 MSSSYDQSSVHN-----IPQSPVSSSES-----APGTIMNGHGG-----RSQQT 321
Db 297 ERSDLOSSVSDRSTSDQDRTTBIGLQGPILSDSDNNPDPSTTSALTSGGTSTTSRASA 356
Qy 322 LDTPKTPGPPALPSVSLSTTSCITALLPSTQHTGDLTSSP-----LSQLSSLSHQ 377
Db 357 SDPTTTPGTTSGTASTTSGSLFSTSLGSSQSPGSSVTTTTPGSTTIGISQSTSGPT 416
Qy 378 SLGAHAALSST-----SHTHASVESASSHQSSATFSTAATSVSSSASGVS 424
Db 417 TTSEPSTTSGTSDTSGPSTTSGPSTTLGTQSTTSGPSTTSGPSTTSGTSTTSSASTSGPS 476
Qy 425 LSSSMNTANSLCLGGTTPASASSSSRAAPLVTSKAPNLPQGVPPPLHNYLVGPGGL 484

Db 477 TSSGTV--STSGQSTSSGTTKSTTSGTTSSG----- 508

QY 485 PAYPIYGYDELOLQSLRPVDYIGIPFAAPTALASDRSLANNP--YPGDVTKFGRGDSA 542

Db 509 -----PSTVSERTLSTSGPSTSGPSTTSGSTVST 539

QY 543 SPAPATTPAQPOQ-----SQSQTHHTAQOFPVNPALPPGYSTGLPYITGMPSAFYQGP 597

Db 540 TPCASTTSGTSTGTPSTSGPSTSGPSTASRSTVSTTSGP--STTSGPSTTSGPSTTSGT 596

QY 598 MFVPPASAKQHGYNLSTPTPPFQOAGSGYGHGYSTGYDDLQCTAGADYSK--GGYAGSS 655

Db 597 KSTTSGPSTTSGKNIST-----VSG-----KLTGTTSATISSAFGNNVTFT 638

QY 656 QAPNKAGSGPGKGVSVSSSTTGLPDMTGVSVNKTQTFDKQGHAGTTPFPFSLPSVLGST 715

Db 639 SKFSNNSGGTSSGKNFSQNTT-----SAANGTTQAVNNGSGSLPTNS-----SS 685

QY 716 GPLASGAAP 724

Db 686 GSSDSSTSP 694

RESULT 12

A53577

ascites sialoglycoprotein 1 - rat (fragments)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 07-Feb-1997

C;Accession: A53577

E;Wu, K.; Fregien, N.; Carraway, K.L.

J. Biol. Chem. 269, 11950-11955, 1994

A;Title: Molecular cloning and sequencing of the mucin subunit of a heterodimeric, bifurcated, type 2 mucin from rat ascites sialoglycoprotein 1

A;Reference number: A53577; MUID:94216302; PMID:8163496

A;Accession: A53577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1630 <WUA>

A;Cross-references: GB:U06746

C;Keywords: glycoprotein

Query Match 6.8%; Score 276.5; DB 2; Length 1630;

Best Local Similarity 20.9%; Pred. No. 2.6e-05;

Matches 205; Conservative 115; Mismatches 362; Indels 301; Gaps 40;

QY 9 TAVNSCPQSLSVLSGSGFGLAPPKVANIATSSOILQKAPSLGQETTFPSQONS--T 66

Db 133 TTTTSHAPRESS-----PP-----STSVIL-----TTTASTEGTSGDT 166

QY 67 SHPTTTTSDWLKPPTSSSVLSHLDFKSOQPSVP-----LSQLSORQHQSOAVT 117

Db 167 GHTNAVITQGSTPATTEISVT-----PSTQKMSPVSTFSTSTQETITLSQSHQTMKTT 221

QY 118 VPPP-----GLESFPSQAKLRSTPGD-----SPSTVNKL-----QLPS 152

Db 222 RNPQTGTEVTITLSSASSDHPSTSPSTPGTAPRTTSTTTTTLTKVLTSLQQLP- 280

QY 153 TTIEINISVHQ-----PPKHILAK----- 174

Db 281 -TGSLGTSTQELATLPSQHGIMKTTSTRTQTTTPEVTTRTLSSASSDHQRETSSQT 339

QY 175 -----RRIPASKIPASAVEMPGSADVTGLVQFALFPGSPSIFEGSA 220

Db 340 TLPSTTTTSHAPRESSPPSTSVILTHGREGTSGDIGHTW--AVTTQGSTPATTEISVT 397

QY 221 PSENSNOIPISLYSKSLEPINTSLMTSAVQNSYTTTSTVITSCSLTSSSINASPAM 280

Db 398 PSTQKMS--PVSTFTSTQETITLSSQSHQTMKTRNPQRTTPEVTITLS----- 448

QY 281 SSSYDOSSVHNRIPIQSPVSSSESAPGTIMNGHGGRSQQTLDTPKT-----TGPPSAL 334

Db 449 ASSSDQVQVET-----TSRATLSFDTTTSHAPSVSSSPSTSTGTSVDGLITAV 501

QY 335 PSVSLPST-----TSCTALLPSTSHQTDGL--TSSP----- 364

Db 502 TTQDSTATTQGSLSSTSSQTLSTVSPPLSTQETSTQELTSSQSHQTMKTTNPTTR 561

QY 365 -----LSQLSSSLSH-QSSLSAHAALSSSTSHTHASVESASSHOSSTATFSTAATSVSSEA 419

Db 562 NTEVTITLSSASSDQVQVETTSQTLTSDATTTSHAPRESSPPSTSDILITMASTEGTSG 621

QY 420 SSGVLSLSSMMNTANSLCLGGTTPA-----SASSSSSRAAPLVTSKGAPNPLPGQVPLLHNQ 475

Db 622 DTGHTMAVTTQ-----GSTPATTEISVTPSTQKMSPVSTFTS-----TQETITLSQSQ 670

QY 476 YLVGPGGLLPAY--PIYGYDELOLQSLRPVDYIGIPFAAPTALASDRSLANNPYGCV 533

Db 671 H---TGGMKTTNRNPTQTTGTEVTITLSSASSDQVQVETTSQTLTSPDTTITSHAP----- 722

QY 534 TKFGRGDSASAPA---TTPAQPOQSQSHHT-----AQQPFVNP 571

Db 723 -----RESSPPSTSDMLTTTASTEGTSGDTGHTTAVTTQGSIPATTTQSLSTTFASQKSTV 778

QY 572 ALP-----PGVSYTG-----LPYYTGMPSAFQYQPTMFVP----- 601

Db 779 STPTTSSITQELSTLPQSOHTGSMRISRPQTTSVTLSLSSPSGSGTPTQTRSVTSSSDE 838

QY 602 --PASAKQHGYNLSTP-----TPFQOASGYGHGISTGYDDLQGTAA-----GDYS 647

Db 839 TNPTSS---GVSNTSPATTEVLTPTSSPESTPGTAPRTTETSTTTTKVLTSLQKLP 895

QY 648 KGYAGSSQAPNK-----SAGSGPGKGVSVSSSTTGLPDMTGVSVNKTQTFDKQFHAGT 702

Db 896 TGSTIGTS--TPTEVTITLSSASSDQVQVETTSQTLTSPDATTTSHAPRE-----SSS 946

QY 703 PPFSL-----PSVLGSGTGLASGAAPGYAPPPF-LHLPLPAHQPHSLHHLLHQD 753

Db 947 PFTSVILTMASTEGTSGDTGHTTAVTTQGSTPATTEISVTPSTQKMSSTVLTSTQE 1006

QY 754 AQSQSGQSRQSPSSLPQKQAKXP 776

Db 1007 LTSSQSQRTSGMGTSSKQATTP 1029

RESULT 13

A40670

nuclear envelope protein POM 121 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C;Accession: A40670

R;Hallberg, E.; Wozniak, R.W.; Blobel, G.

J. Cell Biol. 122, 513-521, 1993

A;Title: An integral membrane protein of the pore membrane domain of the nuclear envelope

A;Reference number: A40670; MUID:93328754; PMID:8335683

A;Accession: A40670

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1199 <HAL>

A;Cross-references: UNIPROT:P52591; GB:221513; NID:G396746; PIDN:CAA7925.1; PID:G396747

F;803-807,845-849,956-960,1010-1014,1047-1051,1076-1080/Region: pentapeptide motif (X-P-);

Query Match 6.8%; Score 274.5; DB 2; Length 1199;

Best Local Similarity 21.8%; Pred. No. 2.2e-05;

Matches 211; Conservative 113; Mismatches 336; Indels 309; Gaps 43;

QY 7 SSTAVNSCPQSLSVLSV-----GSGFGLAP----- 32

Db 275 SSNAPDPCAKETVLNALKKKRTVAEEDQLHLDQENKRRHDSGSGSHSAPEPLVANG 334

QY 33 -----PKMANI---TSSQILD-----OLKAPSLGQFTTT-----PSTQONSTSHPTTT 73

Db 335 VPAAPVFKPSGLKRLASQSSDDHLNKRSTSSVSLTSTCTGIGIFSSRNAITSSVSST 394

QY 74 S-----WDLKPPTSSSVLSHLDFKSOQPSVPVLSQSORQHQH-----Q 114

Db 395 RGVSQLMKRGSTPS-SPFSSPASSRQTPERPAKKTREEPCHOSSSSAPLVTDKSSPGE 453

Qy	115	AVTVPPGCLGSPGQAKLRES--TPGDSPTVNKLLQLPSTTIENISVSHQOPKHKL	172
Db	454	KVTDPATG-----KQSLWTSPPPTPGSSGQRKRKIQLLPSRRGDLTL-----PPPEL--	502
Qy	173	AKRRIPPASKIPASAVEMGSGADVTGLNVQFCALEFGSEPSLSFSGSPASSSENSQI---	229
Db	503	-----GYSITASDLDMERRASLQWFN-----KVLE-----DKTDDASTPATDTSFATSP	547
Qy	230	-----PISLSYKSLSPPLNTSL-----SMTSAVQNSTVTS	260
Db	548	FTLLPTVGPAAASPASLPAPS-SNPLLLESKKMQESPAPSSSEPEEATVAAPSPKTPS	606
Qy	261	VITSCSLTSSSLNAGSPVAMSSSYDQSSVHNRIPYQSPVSSSESAPGTIMNGHGGRSQ	320
Db	607	LL--APLVSP---LTGPLASTSSDSKPTT---TFLGLASASSATPLDTRKAPGVSAQL	657
Qy	321	TLDTPKTTG---PPSALPSVSSLPSTISCTA-----LLPSTSQHTGDLTSS	363
Db	658	CVSTPAATAPSPPTASTLFGMLSPASSSSSLATPGPACASPMFKPIFPATPKSESD--N	714
Qy	364	PLSQLSSLSHQSSLSAHAALSSSTGHT-----HASVESASHOSSATFSTAATS--SSS	418
Db	715	PLPTSSSAATTPAS--TALPTTATATAHTFKPIFESVEPPFAAPMLSPFSLKQTATPAT	773
Qy	419	ASSGVSSSSMNTANSICLGCTPASAS-----SSSSRAAPLVTs-----GKAPPN	463
Db	774	AATSAPLLTLGLTATSTVATGTTTASAKSPVFGFVTTAASTASTIASTSQSILFGGAPPV	833
Qy	464	LPGQVPLLHNQYLVGPGCLLPAYPIYGYDELOMLQSLRLPDYVYIGIPFAAPTALASDRS	523
Db	834	TASSAPALASIFQFGK-PLAPAAASVAGTSFSQ-----SIASSAQT	873
Qy	524	LANNPYGDVTKFGRGDSASPAPATTTPAQPOQSOT--HHTAQQPFVNPALPPGYSVTGL	582
Db	874	AASNSGCGFGGTLTITSAPATT--SQPLTTSNTVTFNLPFASAKXP-----AL	926
Qy	583	PYYTGPMSAFQYGTMTFVPPASAKOHGNLSLTPTPPFOQASGYQHGYSTGYDLDLQGT	642
Db	927	PTYPGANSQPTFGAT-----DGATKPALAPSFSGSSPTFGNSVAS-----	965
Qy	643	AGDYSKGYAGSSOAPNKSAGSGPK-----GVSVSSSTTGLPDMTGVSNNKTTQTFDKQ-	697
Db	966	-----APSAAPAAPAFGGAQPAFGLKASASTFGTTPASTQPAFGSTTSVVFSGS	1015
Qy	698	-----FHAGTTPPFLPSVLGSGTGLASG-----AAPGVAP	728
Db	1016	ATTSGFGAAATTTGTHSGSSSLFSGSTSPFTFG-----GSAAPAGGGGFLSATPTGTS	1072
Qy	729	PPFLHLILPAHQPHQSOLLHHHLPODAQSGS-----GORSQ-----PSSLQ-	772
Db	1073	T-----SGTFSFGSGGSGTGTGTTTSFGGSLSQNTLGAPOSQSPFAFVSGSTP	1119
Qy	773	ASKPAYGNS	781
Db	1120	ESKPVFGGT	1128

RESULT 14

T33369

hypotheical protein H02F09.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T33369

R;Geisel, C.; Harmon, G.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of C. elegans cosmid H02F09.
A;Reference number: Z21330
A;Accession: T33369
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1275 <GEI>
A;Cross-references: UNIPROT:O76602; EMBL:AF077538; PIDN:
A;Experimental source: strain Bristol N2; clone H02F09

C;Genetics:
A;Gene: CESP:H02F09.3
A;Map position: X
A;Introns: 42/1; 78/3; 106/3; 135/2; 161/2; 224/1
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase

Query Match 6.8%; Score 274; DB 2; Length 1275;
Best Local Similarity 22.2%; Pred. No. 2.5e-05;
Matches 170; Conservative 110; Mismatches 337; Indels 150; Gaps 26;

Qy 4 GTGSSHTAVNSCSPOSLSVVGSGFEGELAPPKMANITSSQLDQLKAPSLQGFTTTPTSTQQ 63
Db 427 GSPSTAGTSLASTAVATTETISIGSSSTPLPSQSLSMSLSLTYPSSSTAGATSPATQQ 486

Qy 64 NSTSHPTTTTSDWLKPPT-----SOSSVLHLDFKSQPEPSPVL-----SQLSRQHQQ 112
Db 487 --STKPIGHSMGSPITTVAPGASTSTVLQ----SSTPGTIVTLPGSGSTATAGTSPO 540

Qy 113 SQAV-----TVPPFGLESFPQAKLRSTP---GDSPSTVNKLJLPQLPSTTIENISVSU 162
Db 541 ASTVTVTVDISTVSGSVTSTSQAESSLSTESPTSAAGSISLTVSVSSQPSTYIP----- 594

Qy 163 HQQPQKHUKLAKRRIIPASKI-----PASAVEMPGSADVTGLNVDFGALEFGSEPS--- 213
Db 595 -----VSSASSIYTLGSGTGSTASPGTTSESSGSSTGPSTIGSSASTVT 640

Qy 214 --LSEFGSAPSENSNOPISLYSKLSLEPLNTLSMTSAVQNSTYTTSVITSCLTSS 270
Db 641 GSTVTCASTIGSGTESTIPGSTES-TVSEASTVSGSSVSTVSGSTESTS--AGA-STVSG 697

Qy 271 SLMSASPAMSSSYDOSGVHNRIPYQSPVSSSESAPGTIMNHHGG-GRSOQTLDTPKTTG 329
Db 698 S--TGSTVDSSTISDSTGSTNAPGSTESTVTCSSSVTVSGSTGTPMNSTAGSTNT 755

Qy 330 PPALPSVSLPSTTCTALLPST-----SQTG--DLTSSPLSQLSSLS-----SHQS 377
Db 756 PGSTESTITDGSTVSGSTGTCGTNNPGSTDSTTGISTVSGSSLTIGSTGSTVSGSS 815

Qy 378 SLGAHAALSSSTHTHASVESASSHOSATFSAAATSVSSASSGVSLSSMMTANSLCL 437
Db 816 DMTVTGTSSTPGSTESTVSGAST-MSPSTGSSVETSTSGSSVSTVSGSTSTTQOSTV 874

Qy 438 GGTTPASASSSS-----SRAAPLVTSKGAPPNLPCQVPPLLNXYLVGPCGLLPAYPIYCYDE 494
Db 875 SESSSVTSSESTISQSTGSTITGES----- 900

Qy 495 LQMLORLPVDDYIGIFPAAPTALASDRSLANNPYPGDVTKFGRGDSAPAPATTAPAQPQ 554
Db 901 -----TVFGSTGSTATGSSWTMSASTGSTDTPCGSTESTITGSTVT--GESTVSGSTG 949

Qy 555 QSOQOHTHTAQPFVNPALPPGYSVYGLPYTCMPSAFOYGPTMFVPPASAKOHGNLST 614
Db 950 STITEGSTISESTMVTTVGVSSTGTITGESTVSGSTSTVTGTESTVSGSTESTVSGSTEST 1009

Qy 615 PTPPFQQAAGYGOHGYSTGVDDLTOCTAAGDYSKGYAGSSQAPNKSAAGSGPKGYSVSS 674
Db 1010 PTVP-STVSG-----STG-----STVGESTVSGSTASTSGSGTSGSTEAGSTVSGSS 1056

Qy 675 STTGLPDMTGVSNVKTQTDFDKGFHAGTTPPPFLPSVLSTGTPLAGS 721
Db 1057 AST-VTSSTGSGSTSGBSTV-----SGS-----TVSTVSGSTGSTITG 1092

RESULT 15
E95206
cell wall surface anchor family protein [imported] - Streptococcus pneumoniae (strain TR
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: E95206
R;Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.B.
Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A:Reference number: A95000; MUID:21357209; PMID:11463916 A:Accession: E95206 A:Status: preliminary A:Molecule type: DNA A:Residues: 1-4776 <KUR> A:Cross-references: UNIPROT:Q97P1; GB:AE005672; PIDN:AAK75846.1; PID:G14973269; GSPDB:C A:Experimental source: strain TIGR4 C:Genetics: A:Gene: SP1772

Query Match 6.7%; Score 272.5; DB 2; Length 4776; Best Local Similarity 20.1%; Pred. No. 0.00014; Matches 146; Conservative 120; Mismatches 374; Indels 87; Gaps 8;

QY 2 APTGSGSTAVNSCSPOSLSVLGSGFELAPPKMANITSSQILDQLKAPSLGQFTTTPST 61

DB 2523 ASASASTSASEASTSASASASTSASASASTSASASASTSASVSASTSASEASTSASAS 2582

QY 62 QONSTSHPTTTTWDLKPPTSQSSVLHLDFFKSQPEPSPVLSQLSORQHQOQAVTVPPP 121

DB 2583 ASTSASASTSASASASTSASEASTSASASASTSASASASTSASASASTSASASASTS 2642

QY 122 GLESPFOAKLRESTPCDSPSTVNKLLQLPSTTIENISVHVQOPKHKLAKRRIPPAS 181

DB 2643 ASASASTSASASASTSASASASTSASASASTSASASASTSASASASTSASASASTSAS 2702

QY 182 KIPASAVEMPGSADVTGLNVQFALFPGEPSPSEFGSAPSSNSNOIPISLYSKLSRPP 241

DB 2703 ASASASTSASASASTSASASASTSASASASTSASASASTSASEASTSASTSASTSASES 2762

QY 242 INTSLMWSAVQ-NSVTTSVTITSCLTSSLSNASPVAMSSSYDQSSVHNRIPIYQSPVS 300

DB 2763 ASTSASASTSASASTSASASASTSASASASTSASASASTSASEASTSASASTSASASTS 2816

QY 301 SSESAPGTIWNHGGGRSQTLTPKTTGPPSPALPSVSLPSTTCTALIPSTTSQHTGDL 360

DB 2817 ASTSASASTSASASTSASASTSASASASTSASASASTSASVSASTSASASASTSASEASTS 2876

QY 361 TSFPLQLSSLSHQSSLSAHLGSSSTHSHTHASVESASHOSSATFTTAATSVSSSAS 420

DB 2877 ASASTSASEASTSASASASTSASASASTSASASASTSASASASTSASEASTSASTSASAS 2936

QY 421 SGVLSSSMNTANSLCLGGTTPASASSSSRAAPLIVTSKAPPNLPQGVPELLHNQYLVP 480

DB 2937 TSASEASTSASAS---ASTSASASTSASASASTSASES-----SASAS 2974

QY 481 GGLLPAYPIGYDELOMLQSRLPVYYGIPFAAPTALASRDRSLANNPYFGDVTKFERGD 540

DB 2975 -----ASTSASASTSASES-----ASTSASASTSASES-----AS 2992

QY 541 SASPAPATTAPQOQSQSOTHTTAQPFVNPALPGYVYTGCLPYITGMPSAFQYGTMFV 600

DB 2993 TSASASTSASASASTSASAGSASTSTASASTSASASTSASASTSASASASTSASEAST--- 3049

QY 601 PPASAKQGVNLSPTPPFQOAGYGVGHYSTGYDDLTQGTAGDYSGGYAGSSOAPNK 660

DB 3050 ---SASE---SASTSTASASTSASEASTSASEASTSASASTSASASTSASASTSASAST 3103

QY 661 SAGSGPGKGVSSSTTGLPDMTGSVYNKTTQTFDQKGFHAGTPPPFSLPVLGSGTGLAS 720

DB 3104 SASESASTSASASASTSASASASTSASASTSASASTSASASTSASASTSASASTSASASTS 3156

QY 721 GAAPGYA 727

DB 3157 ASTSASA 3163

Search completed: January 31, 2005, 17:47:30
Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 31, 2005, 17:38:16 ; Search time 206 Seconds
(without alignments)
2195.362 Million cell updates/sec

Title: US-10-509-307-1
Perfect score: 4055
Sequence: 1 MAPETGSSAVNCSPOSLS.....LQPKSQASKPAYGNPWTN 786

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3902	96.2	757	2 Q9P237	Q9P237 homo sapien
2	3214.5	79.3	1132	2 Q812D6	Q812D6 mus musculus
3	3214.5	79.3	1132	2 Q91VX2	Q91VX2 mus musculus
4	3083	76.0	597	2 Q8NC94	Q8NC94 homo sapien
5	2902	71.6	700	2 Q99K40	Q99K40 mus musculus
6	1746.5	43.1	583	2 Q9P0H6	Q9P0H6 homo sapien
7	1599	39.4	1087	2 Q9BTU3	Q9BTU3 homo sapien
8	1581	39.0	1107	2 Q80X50	Q80X50 mus musculus
9	1581	39.0	1112	2 Q8BJ01	Q8BJ01 mus musculus
10	1536	37.9	363	2 Q6UWR4	Q6UWR4 homo sapien
11	1536	37.9	363	2 AAQ89045	AAQ89045 homo sapi
12	1520	37.5	1067	2 Q8CI67	Q8CI67 mus musculus
13	1507.5	37.2	1105	2 Q8KI02	Q8KI02 mus musculus
14	1433	35.3	263	2 Q6PK34	Q6PK34 homo sapien
15	1433	35.3	263	2 AAH07890	AAH07890 homo sapi
16	1409.5	34.8	1035	2 Q812D5	Q812D5 mus musculus
17	1392	34.3	311	2 Q6Y2W0	Q6Y2W0 gallus gall
18	1392	34.3	311	2 AAP21493	AAP21493 gallus gall
19	1384.5	34.1	305	2 Q6Y2W4	Q6Y2W4 gallus gall
20	1384.5	34.1	305	2 AAP21489	AAP21489 gallus gall
21	1379	34.0	311	2 Q6Y2V8	Q6Y2V8 gallus gall
22	1379	34.0	311	2 AAP21495	AAP21495 gallus gall
23	1374.5	33.9	312	2 Q6Y2W1	Q6Y2W1 gallus gall
24	1374.5	33.9	312	2 AAP21492	AAP21492 gallus gall
25	1370	33.8	317	2 Q6Y2V9	Q6Y2V9 gallus gall
26	1370	33.8	317	2 AAP21494	AAP21494 gallus gall
27	1360.5	33.6	312	2 Q6Y2V7	Q6Y2V7 gallus gall
28	1360.5	33.6	312	2 AAP21496	AAP21496 gallus gall
29	1356.5	33.5	312	2 Q6Y2V6	Q6Y2V6 gallus gall
30	1356.5	33.5	312	2 AAP21497	AAP21497 gallus gall
31	1353.5	33.4	307	2 Q6Y2W3	Q6Y2W3 gallus gall

32 1353.5 33.4 307 2 AAP21490
33 1353 33.4 306 2 Q6Y2W2
34 1353 33.4 306 2 AAP21491
35 1295 31.9 360 2 Q6Y2W7
36 1295 31.9 360 2 AAP21486
37 1248.5 30.8 983 1 Y144_HUMAN
38 1234.5 30.4 983 2 Q8BU53
39 1234.5 30.4 1014 2 Q8BIT6
40 1233.5 30.4 983 2 Q812D4
41 1213 29.9 1015 2 Q8BIW4
42 1135 28.0 389 2 Q8BZ69
43 1092 26.9 496 2 Q8OU73
44 1088 26.8 398 2 Q9UGL3
45 1027 25.3 408 2 Q9UGL4

ALIGNMENTS

RESULT 1
Q9P237
ID Q9P237 PRELIMINARY; PRT; 757 AA.
AC Q9P237;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE KIAA1491 protein (Fragment).
GN Name=KIAA1491;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20277482; Pubmed=10819331;
RA Nagase T., Kikuno R., Ishikawa K., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:143-150(2000).
DR EMBL; AB040924; BAA96015.1; -.
FT NON_TER
SQ SEQUENCE 757 AA; 78010 MW; A037345123622D57 CRC64;

Query Match 96.2%; Score 3902; DB 2; Length 757;
Best Local Similarity 99.9%; Pred. No. 3.2e-153;
Matches 756; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 30 LAPPKMANITSSQILDQLKAPSLGQFTTPTSTQONSTSHPTTTTSDWKPKPTSSQSVLSH 89
Db 1 LAPPKMANITSSQILDQLKAPSLGQFTTPTSTQONSTSHPTTTTSDWKPKPTSSQSVLSH 60
Qy 90 LDFKSQPEPSPVLSQLSORQHQSOAVTVPPGLESPPSOAKLRETFGSPSTVKNLLQ 149
Db 61 LDFKSQPEPSPVLSQLSORQHQSOAVTVPPGLESPPSOAKLRETFGSPSTVKNLLQ 120
Qy 150 LPSTTTIENISVHVQPOPKHIKLAKRRIIPASKIPASAVEMPGSADVTGLNVQFGALEFG 209
Db 121 LPSTTTIENISVHVQPOPKHIKLAKRRIIPASKIPASAVEMPGSADVTGLNVQFGALEFG 180
Qy 210 SEPSLSEFGSAPSENSENQIPISLYSKSLSEPLNTSLMTSAVQNSTYTTTTSVITSCSLTS 269
Db 181 SEPSLSEFGSAPSENSENQIPISLYSKSLSEPLNTSLMTSAVQNSTYTTTTSVITSCSLTS 240
Qy 270 SSLNASPVMSSSYDOSSVHNRIPOSVPSSSEAPGTIMNGHGGGRSQOTLDPKTTG 329
Db 241 SSLNASPVMSSSYDOSSVHNRIPOSVPSSSEAPGTIMNGHGGGRSQOTLDPKTTG 300
Qy 330 PPSALPSVSLPSTTCTALLPSTSOHTGDLTSSPLSQLSSLSHSHOSSLSAHAALSSST 389
Db 301 PPSALPSVSLPSTTCTALLPSTSOHTGDLTSSPLSQLSSLSHSHOSSLSAHAALSSST 360
Qy 390 SHTHASVESASHSQSSATFTAATSVSSSSASSGVLSSSSMNTANSCLGCTPPASASSSSS 449

Db	361	SHTHASVESASHQSSATESTAAATSVSSASSGVSLSSMTANSLCLGGTPASASSSS	420
Qy	450	RAAPLVTSKAPNLPQGVPPLLHNOYLVPGLLPAYPIYGYDELOMLQSLPVDYVGI	509
Db	421	RAAPLVTSKAPNLPQGVPPLLHNOYLVPGLLPAYPIYGYDELOMLQSLPVDYVGI	480
Qy	510	PFAAPTALASRDSELANNPVGDVTKFGRGDSASAPATTAPQOQSQSQTHTTAQPPFV	569
Db	481	PFAAPTALASRDSELANNPVGDVTKFGRGDSASAPATTAPQOQSQSQTHTTAQPPFV	540
Qy	570	NPALPCGYSTGLPYITGMPSAFQGYTGMFVPASAKQHGVMNLSTPTTTPPQOASGYGQH	629
Db	541	NPALPCGYSTGLPYITGMPSAFQGYTGMFVPASAKQHGVMNLSTPTTTPPQOASGYGQH	600
Qy	630	YSTGYDDLTOGTAAGDYSGGYAGSSQAPNKSAGSGPGKGVSVSSTTGLPDMTGSVYNK	689
Db	601	YSTGYDDLTOGTAAGDYSGGYAGSSQAPNKSAGSGPGKGVSVSSTTGLPDMTGSVYNK	660
Qy	690	TQTFDKQGFHAGTPPPPSLPSVLGSGTGLASGAAPGYAPPFLHILPAHQPHSOLLHHH	749
Db	661	TQTFDKQGFHAGTPPPPSLPSVLGSGTGLASGAAPGYAPPFLHILPAHQPHSOLLHHH	720
Qy	750	LPQDAQSGSGQSGOPSSLOPKSQASKPAYGNSPYWTN	786
Db	721	LPQDAQSGSGQSGOPSSLOPKSQASKPAYGNSPYWTN	757
RESULT 2			
Qy	Q812D6	PRELIMINARY; PRT; 1132 AA.	
Db	Q812D6	PRELIMINARY; PRT; 1132 AA.	
Qy	Q812D6	(TrEMBLrel. 24, Created)	
Db	Q812D6	(TrEMBLrel. 24, Last sequence update)	
Qy	Q812D6	(TrEMBLrel. 26, Last annotation update)	
Db	Q812D6	(TrEMBLrel. 26, Last annotation update)	
Qy	Q812D6	Lingerer protein-1.	
Db	Q812D6	Lingerer protein-1.	
Qy	Q812D6	Mus musculus (Mouse).	
Db	Q812D6	Mus musculus (Mouse).	
Qy	Q812D6	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Db	Q812D6	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Qy	Q812D6	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
Db	Q812D6	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
Qy	Q812D6	NCBI_TaxID=10090;	
Db	Q812D6	NCBI_TaxID=10090;	
Qy	Q812D6	SEQUENCE FROM N.A.	
Db	Q812D6	SEQUENCE FROM N.A.	
Qy	Q812D6	MEDLINE=22412137; PubMed=12524348;	
Db	Q812D6	MEDLINE=22412137; PubMed=12524348;	
Qy	Q812D6	Kuniyoshi H., Baba K., Ueda R., Kondo S., Awano W., Juni N.,	
Db	Q812D6	Kuniyoshi H., Baba K., Ueda R., Kondo S., Awano W., Juni N.,	
Qy	Q812D6	Yamamoto D.;	
Db	Q812D6	Yamamoto D.;	
Qy	Q812D6	"lingerer", a Drosophila gene involved in initiation and termination of	
Db	Q812D6	"lingerer", a Drosophila gene involved in initiation and termination of	
Qy	Q812D6	copulation, encodes a set of novel cytoplasmic proteins."	
Db	Q812D6	copulation, encodes a set of novel cytoplasmic proteins."	
Qy	Q812D6	Genetics 162:1775-1789(2002).	
Db	Q812D6	Genetics 162:1775-1789(2002).	
Qy	Q812D6	EMBL; AF276965; AAO23024.1; -.	
Db	Q812D6	EMBL; AF276965; AAO23024.1; -.	
Qy	Q812D6	MGI; 1916176; Ubp2.	
Db	Q812D6	MGI; 1916176; Ubp2.	
Qy	Q812D6	InterPro; IPR000449; UBA.	
Db	Q812D6	InterPro; IPR000449; UBA.	
Qy	Q812D6	InterPro; IPR009060; UBA_like.	
Db	Q812D6	InterPro; IPR009060; UBA_like.	
Qy	Q812D6	Pfam; PF00627; UBA; 1.	
Db	Q812D6	Pfam; PF00627; UBA; 1.	
Qy	Q812D6	SMART; SM00165; UBA; 1.	
Db	Q812D6	SMART; SM00165; UBA; 1.	
Qy	Q812D6	SEQUENCE 1132 AA, 117935 MW, 48F091F992E3659A CRC64;	
Db	Q812D6	SEQUENCE 1132 AA, 117935 MW, 48F091F992E3659A CRC64;	
Query Match			
Best Local Similarity 79.0%; Pred. No. 1e-124; Length 1132;			
Matches 636; Conservative 46; Mismatches 98; Indels 25; Gaps 9;			
Qy	1	MARGTSGSTAVNSCPQSLSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQPTTTPS	60
Db	334	MARGTSGSTAVNSCPQSLSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQPTTTPS	393
Qy	61	TQONST-SHPTTTTNDLKPPTSSQSVLGHLPKSPVLSQSQOQHSQAVTVP	119
Db	394	AQONDATSPATTAADWLKPSAPQPSVLSRLDFKSPSPVLSQSQOQHSQAVTVP	453
Qy	120	PGLESFPSQAKLRSTPGDPSVTNKLQLPPTTIENTSVSHQPPQPHIKLAKRRIPP	179
Db	454	PGLESFPSQAKLRSTPGDPSVTNKLQLPPTTIENTSVSHQPPQPHIKLAKRRIPP	512

RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP	[2]
RN	SEQUENCE FROM N.A.
RC	STRAIN-Mix FVB/N;
RC	TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RC	Strauberg R.;
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL	EMBL; BC007179; AA071179.1; --
DR	MGD; MGI:1916176; Ubpap2.
DR	InterPro; IPR000449; UBA.
DR	InterPro; IPK009060; UBA_like.
DR	Pfam; PF00627; UBA; 1.
DR	SMART; SM00165; UBA; 1.
SO	SEQUENCE 1132 AA; 117965 MW; ECF8E72C9134BB38 CRC64;
Query Match 79.3%; Score 3214.5; DB 2; Length 1132;	
Best Local Similarity 79.0%; Pred. No.1e-124;	
Matches 636; Conservative 46; Mismatches 98; Indels 25; Gaps 39;	
QY	1 MAPGTGSSATVNSCSPOSLSVLGSGFGEIAPPKWANITTSOIIDLKAPSLGOFTTTPS 60
DB	: : : : : : : : : : : : : : : : : : : :
DB	334 MAPGTANTSTASSYPQSLSVLGSGFGEILPQSNMVNISQIIDLKULPGCLSPFPAASS 393
QY	61 TQQNST--SHPTTTTSDWLKPPTSQSSVLSHLDFKSQPESPVLSQLSORQHQQAVTVP 119
DB	: : : : : : : : : : : : : : : : : : : :
DB	394 AQNDQTASPPATTAADWLKPSAPOSVLSRLDFKSQPEPVLSQLSORQHQQAVTVP 453
QY	120 PGLSEPPSOAKURESTPGDSPSTVNKLQLDPSTTIENISVSVHQPOPKHKLAKRRIPP 179
DB	: : : : : : : : : : : : : : : : : : : :
DB	454 PGLSESPSLAKPRETAGDGPSTVSRLLQLPNMTVENI-VSAHQPOPKHKLPKRVRVP 512
QY	180 ASKIPASAVRMGPSADVTGLNVQGALEFGSEPLSEFSGAPS--SENSNQIPISLYSKSL 238
DB	: : : : : : : : : : : : : : : : : : : :
DB	513 ASKVPSGAVEMPGSSDVTGLNVQGALEFGSEPLSEFSGAASENSNQIPISLYPKSL 572
QY	239 SEPLNTSLSMTSVAQNSTYTTSVTITSSLSLSSLNINSPAMSSSYQSSVHNRIPTYQSP 298
DB	: : : : : : : : : : : : : : : : : : : :
DB	573 SEPLNASFPMTSAVQSSTYTTSVTTSLSALSSSTSPVTTSSSYQSSVHTFIAYQSS 632
QY	299 VSSSESAPGITMNGHGGRGSOQLDT-----PKTTGPPSALPSVSSLPTSTCTALLPS 352
DB	: : : : : : : : : : : : : : : : : : : :
DB	633 ASPPDSPAAGVANGHGGRGSOHTVDTTSSVPAPKKT-DPSALPSVTLPGPASCTALLPS 691
QY	353 TSQHT-----GDLTSSPLSOLSSLSSSHOSLL-SAHAAALSSSTSHTHASVESASS 401
DB	: : : : : : : : : : : : : :
DB	692 SAQHTATLPSLTPAAEELSSPSLSQSSLSUGHQNSMTSAHAATKSTSTPTHASVESTA- 750
QY	402 HQSSATESTAAITSVSSSAGSGVSLSSSMNTRANSICLAGTTPASASSSSRAAPLVTSKAP 461
DB	: : : : : : : : : : : : : :
DB	751 --SSAAESAANTSAPASPSSGVLPWGSMTSVSSLCIGTTVSPSSSTRATALVTSKAP 808
QY	462 PNLPQGVPPLLHNQYLVGPGGLPAYPIYGYDELOMLQSLRPVDYGYGIFPAAAPTALASRD 521
DB	: : : : : : : : : : : : :
DB	809 PNLPQGVPPLLHNQYLVGPGGLPAYPIYGYDELOMLQSLRPMDYGYGIPFAAPTALASRD 868
QY	522 RSLANNPYPGDVTKFGRGDSASAPATTTPAQPOQSOSTHHTAQOFPFNALPGYSYTG 581
DB	: : : : : : : : : : : : : :
DB	869 GNLANNPYGSDVTKFGRGDSASAPPTTPAQAOQSOSTHHTAQOQPFNLPGLPPEGYSYTG 928
QY	582 LPYYTGMPSAFQYGMTTFVPPASAKOHGVNLSTPTTPFQAQSGYGOHGYSTGYDDLTOGT 641
DB	: : : : : : : : : : : : :
DB	929 LPYYTGVPSAFQYGMTTFVPTPSAKOHGVNLSTPTTPFQAQSGYGOHAYSTGYDDLTOGT 988
QY	642 AAGDYKGGYAGSSQAPNKAGSGPGKGVSVSSSTTGLPDMTGSVYNKTTQTDFKQGFPHAG 701

Db	989	AAAGDYTKGGYGGSSQAPNKSTGSGPGKGVSVSSG-TGLPDMTGVSVNKTQTFDKQGFHAG	1047
Qy	702	TPPFSLPSVLGSGTGPLASGAAPGYAPPPPLHLTPAHQQPHSOLLHHLLPQDAQSGSGQR	761
Db	1048	TPPFSLPSALGSGTGPLADNACGYAPAPFLHIMPAPHQQPHSOLLHHLLQODAPSGGQR	1107
Qy	762	SQPSSLPQKSQASKPAYGNSPYWTN	786
Db	1108	SQPSSLPQKSQASKPTYGSAFYWTN	1132
RESULT 4			
ID	Q8NC94	PRELIMINARY; PRT; 597 AA.	
AC	Q8NC94;		
DT	01-OCT-2002 (T-EMBLrel. 22, Created)		
DT	01-OCT-2002 (T-EMBLrel. 22, Last sequence update)		
DT	01-MAR-2003 (T-EMBLrel. 23, Last annotation update)		
DE	Hypothetical protein FLJ90403.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Isegai T., Ota T., Nishikawa T., Hayaashi K., Otsuki T., Sugiyama T.,		
RA	Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saïto K.,		
RA	Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,		
RA	Masuko Y., Ono T., Okano K., Yoshioka Y., Aotsuka S., Sasaki N.,		
RA	Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AK074884; BAC11266.1; --		
DR	Genew; HGNC:14185; UBA2.		
SQ	SEQUENCE 597 AA; 60780 MW; DBDB70598D935F1E CRC64;		
Query Match			
Best Local Similarity 99.7%; Pred. No. 1.4e-119;			
Matches 595; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
Qy	190	MPGSAADVTGLNVQFGALEFGSPSLSEFGSAPSSSENSNOIPISLYSKSLSEPLNTLSMT	249
Db	1	MPGSAADVTGLNVQFGALEFGSPSLSEFGSAPSSSENSNOIPISLYSKSLSEPLNTLSMT	60
Qy	250	SAVONSTYTTVTTSCTSLTSSLSNASPVAMSSSYDQSSVHNRIPYQSPVSSSESAPGTI	309
Db	61	SAVONSTYTTVTTSCTSLTSSLSNASPVAMSSSYDQSSVHNRIPYQSPVSSSESAPGTI	120
Qy	310	MNGHGGGRSQOQLDTPKTTGPPSALPSVSLPSTTCTALLPSTSOHTGDLTSSPLSQLS	369
Db	121	MNGHGGGRSQOQLDTPKTTGPPSALPSVSLPSTTCTALLPSTSOHTGDLTSSPLSQLS	180
Qy	370	SSLSSHQSLSAHAALLSSSTSHTHASVESASHQSATSFTATSVSSSASGVSLSSSM	429
Db	181	SSLSSHQSLSAHAALLSSSTSHTHASVESASHQSATSFTATSVSSSASGVSLSSSM	240
Qy	430	NTANSLCLGTPASASSSSSRAAPLVTSCAPENLPOGVVPLLHNQYLVPGLLPAYPI	489
Db	241	NTANSLCLGTPASASSSSSRAAPLVTSCAPENLPOGVVPLLHNQYLVPGLLPAYPI	300
Qy	490	YGYDELOMLQSLPVDYIYGFPAAPTALASRDRLANNPYPGDVTKFGRGDSASPAPATT	549
Db	301	YGYDELOMLQSLPVDYIYGFPAAPTALASRDRLANNPYPGDVTKFGRGDSASPAPATT	360
Qy	550	PAQPOQSQSQTHHTAQOQFVNALPGYISYTGLPYTTGMPSAFOYQPTWFPVPASAKQHG	609
Db	361	PAQPOQSQSQTHHTAQOQFVNALPGYISYTGLPYTTGMPSAFOYQPTWFPVPASAKQHG	420
Qy	610	VNLSTPTPPFQOASGVGHGYSTGYDDLTLQGTAAAGDYSKGGYAGSSOAPNKSAGSGPGKG	669
Db	421	VNLSTPTPPFQOASGVGHGYSTGYDDLTLQGTAAAGDYSKGGYAGSSOAPNKSAGSGPGKG	480
Qy	670	VSVSSSTTCLGPOMTGSVYNKTTQTFDKQGFHAGTPPPFSLPSVLGSGTGPLASGAAPGYAPP	729

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Db 481 VSVSSSTGLPDMTGSVYKNTQTFDKQGFHAGTTPFPFSLPSVLGSLGSLASGAAPGYAPP 540
|||||
QY 730 PFLHILPAHQPHSOLLHLHLLPQDAQSGQSGQSQSSLPQKSAQKPAYGNSPYWTN 786
|||||
Db 541 PFLHILPAHQPHSOLLHLHLLPQDAQSGQSGQSGQSSLPQKSAQKPAYGNSPYWTN 597
|||||

RESULT 5
Q99K40 PRELIMINARY; PRT; 700 AA.
ID Q99K40
AC Q99K40
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Ubp2 protein (fragment).
GN Name=Ubp2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bourfard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005482; AAH05482.1; -.
DR MGD; MGI:1916176; Ubp2.
FT NON_TER 1
SQ SEQUENCE 700 AA; 71456 MW; DD2C8296DCASFBED CRC64;

Query Match 71.6%; Score 2902; DB 2; Length 700;
Best Local Similarity 80.9%; Pred. No. 4.7e-112;
Matches 571; Conservative 39; Mismatches 72; Indels 24; Gaps 8;

QY 99 SPVLSOLSOHQSOAVTVPPGLESPSOAKLRESTPGDSPSTVKNKLLQLPSTTIENI 158
|||||
Db 1 SPVLSOLSOHQSOAVTVPPGLESPSOAKLRESTPGDSPSTVKNKLLQLPSTTIENI 60
|||||

QY 159 SVSVHQPQPKHKLAKRRIPPPASKIPASAVEMPGSDVTGLNVQCALEFGSEPLSEFG 218
|||||
Db 61 -VSAHQPPKHKLKRRIPPPASKIPASAVEMPGSDVTGLNVQCALEFGSEPLSEFG 119
|||||

QY 219 SAPS-SENQNPISLYKSLSEPLNTSLSMYSAVQNSYTTVTSVLTSSLTSSLSNASP 277
|||||
Db 120 SAASASSENSQNPISLYKSLSEPLNAPFMTSAVQNSYTTVTSVLTSSLTSSLSNASP 179
|||||
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```
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RC MEDLINE=22388257; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Collins K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Wang J., Hsieh L.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohiryuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schermer A., Schein J.E.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain;
RC STRAIN=C57BL/6J; TISSUE=Brain;
RL Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC050910; AAHE0910.1; -
DR MGD; MGI:1921633; 4392431F02Rik.
DR InterPro; IPR000449; UBA.
DR InterPro; IPR009060; UBA-like.
DR Pfam; PF00627; UBA; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00303; UBA; 1.
DR SEQUENCE 1107 AA; 116798 MW; F4A4FB502B619C51 CRC64;
SQ
Query Match 39.0%; Score 1581; DB 2; Length 1107;
Best Local Similarity 45.6%; Pred. NO. 2e-57;
Matches 380; Conservative 112; Mismatches 215; Indels 126; Gaps 31;
QY 3 PGTGSGTAVNCSCPSGLSVGSGFGEALAPPRMANITSSQILDQK-APSLGQTTTPST 61
Db 347 PASGS-----TSHHSMVSMGLKGFQDVGGEAKGTTGSGFLEQFKTAQALAA---- 397
QY 62 QQNSTSHPTTTSDWKLPFTSSSVLSHLDFKSPSPVLSQLSQRO----- 109
Db 398 -QHSQSGSTTTSDWM-GSTTQPSLVQVLDKAND-STVHSPTFKRQAFPSSTMMEVF 454
QY 110 -QHQSQAV---TVRPPGLESPFOAKLRETPGDSPTVKNLQLPPTTIENISVSHQ 164
Db 455 LQEKPAVATSTAAAPPPSPSPSKS---TSAPQSPGSDNDQSSSP-----Q 499
QY 165 POPKHILAKRIPPAKIPASAVEMPGADVTGLNVQGALEFSEPSLSEFGSAP-SS 223
Db 500 PAQKQLKQKQKTSKTLTKIPALAVEMPGSADISGLMLQFALQFSGEVLSDYESTPTIS 559
QY 224 ENSNQIPISLXSKLEPNTLSMTSAVQNSYTTTSTVITSCSLTSSSLNSASPVAMSS 283
Db 560 ASSSQAPSSLYTASGSSSTVSNSQS--QESYQSGPQISTYITSON-NAQGPI----- 611
QY 284 YDQSSVHNRIYQSPVSSSESAPGT-IMNGHGGRSQQLDTPKTTGP-----PSALPSV 337
Db 612 YEQESTQTR-RYPSSISSSPQKDLTKQNGFSSVQATQLTQTSVEGATGSAVKSESPT 670
QY 338 SSIPSPS-----TTSCTALLPSTSQ-----HTGDLTSSPLSQLSSSLSHQSLSAHAL 385
Db 671 SSIPSLNETVPAASLLTANQSSSLGSLSHTEIEPTITTTQHSALSTQQNTLSSSTSS 730
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QY 386 SSSSTHT--HASYVES-ASSHQSSATFSTAATSVSSASSGVSLSSSMNTANSILCGTTPA 442
Db 731 GRTSTSTLLHTSVSESEANLHSSSTFTSTTSVAPPV-VSVSSSLHSGSLGLSLGSN 789
QY 443 SASSSSRAAPLVTSGKAPPNLPQGVPPPLHQQYLVGPGGLLPAYP--IYGVDELQMLQS 500
Db 790 STVTASTRSRVATTSKAPNLPQGVPPPLPNPYIMAP-GLLHAYPPQVYGVYDQLMLQT 848
QY 501 RLPVDYVIGPFAAPTA-LASRRSLANNYPGQVTKFEGRDSASAPATTTPAQPOQSOSQ 559
Db 849 RFLDYYSIFPFTTTLTGRDGLSNPYSGLTKFGRDASSAPATTLAQPOQNQTQ 908
QY 560 THHTAQOPFVNPALPGYSYVTLPPYTT--GMPSAFYGTGTMF-VPPASAKQHGYNLS-- 613
Db 909 THHTTQOTFLNPALPGYSYVTLPPYTTGVPGLPSTFYGPAVFPVAPTSSKQHGNNVSN 968
QY 614 TPTPPFQOASGYGQHGYSYTGVDLDTQGTAAAGDYSGGYAGSSQAPNKSAGSGPGKGVSVS 673
Db 969 ASATFPQPSGYSYSHGNT-----GVSVT 992
QY 674 SSTTGLDMTGSYNYKT-OTFDKQGHAGTP-PFSLPSVLGSTGLASGAAPGYAPPPF 731
Db 993 SSNTGVPDISGVSYSKTTQSGFEKQGHSGTTPAASFNLPSALSGGPINPATAAAYPPAPF 1052
QY 732 LHILPAHQPHQSQHLHHLHPQDAGSGSGQSGSSSQPSKQSKAPAYGNSPYW 784
Db 1053 MHILTPHQPHQSQHLHHLHPQDAGSGSGQSGSSSQPSKQSKAY-NSYSW 1104
RESULT 9
QY Q8BJ01 PRELIMINARY; PRT: 1112 AA.
Db Q8BJ01
AC Q8BJ01;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
DE library, clone:CI30046J04 product:NICE-4 PROTEIN homolog.
GN Name=4932431F02Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=99279253; PubMed=10349636;
RX Carninci P., Hayashizaki Y.;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RC MEDLINE=21085660; PubMed=11217851;
RX RIKEN FANTOM Consortium;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20493374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
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Db 129 SPFSQAKLRETFGDSPTVKNLLQLPSTTIENISVSVHQPOPKHKLAKRIPPASKIP 188
QY 185 ASAVEMPGADVTGLNVQFALFPGSEPLSFGAPSENSNQIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGADVTGLNVQFALFPGSEPLSFGAPSENSNQIPISLYSKSLSEPLNT 248
QY 245 SLSMTSAVQNSTVTTSVITSSCSLTSSLSNSASFPVAMSSSYDOSSVHNRIPIQSPVSSSES 304
Db 249 SLSMTSAVQNSTVTTSVITSSCSLTSSLSNSASFPVAMSSSYDOSSVHNRIPIQSPVSSSES 308
QY 305 APTGIMNGHGGRSQOTLDT 324
Db 309 APTGIMNGHGGRSQOTLDS 328
RESULT 11
ID AAQ89045 PRELIMINARY; PRT; 363 AA.
AC AAQ89045;
DT 02-MAR-2004 (T-EMBLrel. 27, Created)
DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)
DE UPAP2.
GN Homo sapiens (Human).
OS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12975309;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eason D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seehagiri S., Simmons L., Singh J., Smith J., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RA "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A
RT Bioinformatics Assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL: AY358682; AAQ89045.1; -.
SQ SEQUENCE 363 AA; 38824 MW; A7B4524E0AEBD45D CRC64;
Query Match 37.9%; Score 1536; DB 2; Length 363;
Best Local Similarity 96.2%; Pred. No. 4.5e-56;
Matches 308; Conservative 3; Mismatches 7; Indels 2; Gaps 1;
QY 7 SSTAVNSCS--PQSLSSVLGSGFGELAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 64
Db 9 NSVLIRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQKAPSLGQFTTTPSTQON 68
QY 65 STSHPTTTTSDWKLPPTSSQSVLSHLDFKSPQPEPVTLSQSRQHQSOQAVTVPBGLLE 124
Db 69 STSHPTTTTSDWKLPPTSSQSVLSHLDFKSPQPEPVTLSQSRQHQSOQAVTVPBGLLE 128
QY 125 SPFSQAKLRETFGDSPTVKNLLQLPSTTIENISVSVHQPOPKHKLAKRIPPASKIP 184
Db 129 SPFSQAKLRETFGDSPTVKNLLQLPSTTIENISVSVHQPOPKHKLAKRIPPASKIP 188
QY 185 ASAVEMPGADVTGLNVQFALFPGSEPLSFGAPSENSNQIPISLYSKSLSEPLNT 244
Db 189 ASAVEMPGADVTGLNVQFALFPGSEPLSFGAPSENSNQIPISLYSKSLSEPLNT 248
QY 245 SLSMTSAVQNSTVTTSVITSSCSLTSSLSNSASFPVAMSSSYDOSSVHNRIPIQSPVSSSES 304
Db 249 SLSMTSAVQNSTVTTSVITSSCSLTSSLSNSASFPVAMSSSYDOSSVHNRIPIQSPVSSSES 308
QY 305 APTGIMNGHGGRSQOTLDT 324

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Db 309 APTGIMNGHGGRSQOTLDS 328
RESULT 12
ID O8CIG7 PRELIMINARY; PRT; 1067 AA.
AC O8CIG7;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Nice-4 protein homolog, isoform 2.
GN Name=4932431F02Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ugin T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL: BC023906; AAH23906.1; -.
DR MGI:1921633; 4932431F02Rik.
DR InterPro; IPR000449; UBA_like.
DR InterPro; IPR009060; UBA_like.
DR Pfam; PF00627; UBA; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS50030; UBA; 1.
SQ SEQUENCE 1067 AA; 112451 MW; FBE932FB2D4DBB6F CRC64;
Query Match 37.5%; Score 1520; DB 2; Length 1067;
Best Local Similarity 45.2%; Pred. No. 6.3e-55;
Matches 363; Conservative 109; Mismatches 207; Indels 124; Gaps 29;
QY 3 PGTSSTAVNSCS--PQSLSSVLGSGFGELAPPKMANITSSQILDQK-APSLGQFTTTPST 61
Db 327 PASGS-----TFSHHSMVSNLKGFGDVGKSGSTGSGFLEQFKTAQALAA---- 377
QY 62 QONSTSHPTTTTSDWKLPPTSSQSVLSHLDFKSPQPEPVTLSQSRQHQSOQAVTVPBGLLE 109
Db 378 -QHSQSGSTTTSSWDM-GSTTQSPSLVQYDLKSAND-STVHSPFTKRAFTTSSTMEVF 434
QY 110 -QHSQSAV-----TVPPGLESPFSQAKLRETFGDSPTVKNLLQLPSTTIENISVSVHQ 164
Db 435 LQKPPAVATSTAAPPPSPLEFSKSKS---TSAPQMSFGSSDNQSSSP-----Q 479
QY 165 PQPKHKLAKRIPPASKIPASAVEMPGADVTGLNVQFALFPGSEPLSFGAPSENSNQIPISLYSKSLSEPLNT 223

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480 PAQKLLKQKKTSLSKIPALAVEMPGSADISGLNLFQFGLQFSGSPVLSDYESTPTTS 539
224 ENSNQIPISLYSKLSBLPLNTSLMTSAVQNSTYTTTSVITSSCSLTSSLSASPVAMSSS 283
540 ASSSQAPSSLYTSTASESSSTVSNQS--QESGYQSGPIQSTTYTSQN-NAQGPL----- 591
284 YQSSVHNRIPIYQSPVSSSESAPGT-IMNGHGGGRSQOTLDTPTKTPG-----PSALPSV 337
592 YEQRSTQTR-RYPSSISSSPQKDLTQAKNGFSSVQATQLOTTQSVGATGSAVKSESPT 650
338 SSILPS---TTSCCTALLPSTQ-----HTGDLTSSPLSQLSSLSHSSQSSLSAHAAL 385
651 SSIPSLNETVPAASLLTANQHSSLSGLSHTBEIPNTTTTQHSSALSTQNTLSSTSS 710
386 SSSTSHT--HASVES--ASHQSSATFTSTAATSVSSSSAGSVLSSSMNTANSCLGCTPA 442
711 GRTSTSTLLHTSVESSEANLHSSSTFTSTSTVSAPPVPV-VSVSSLSNCSGLSLGSGN 769
443 SASSSSRAPLVTSGKAPENLPQGVPPPLLNQVLPGLLPAYP--IYGYDELOMLQS 500
770 STVTASTRSSVATTSGKAPENLPQGVPPPLLPNPYIMAP-GLLHAYPPQVGYDDQLQOT 828
501 RLPVDYVYGIFFAAPT-AASRDRLANNPVGDTKFGSDSASPAPATTPAQPOQSSQSO 559
829 RFLDYYSIFPPTPTTLCRDCGLASNPVSGDLTKFGRGDSSAPATTLAQPOQNTQ 888
560 THHTAQOQFVNPAALPPGYSTGLPYTT---GMPSAFOYGTMPF-VPPASAKQHGVLNLS-- 613
889 THHTTQOTFLNPAALPPGYSTGLPYTTGVCLPSTFYQVPAVPVAPTSKQHGVLNLSVN 948
614 TPTPPFOQAGYQGHGYSYTGVDLDTQGTAAAGDYSKGGYAGSSQAPNKSAGSGPKGVSVS 673
949 ASATPPFOQPSGSGHGYNT-----GVSVT 972
674 SSTTGLPDMTGSVYNTKOTFDKQGFHAGTP-PPSLPSVLGTCPLASGAPGAPPPFL 732
973 SSNTGVPDISGSYKTSQSEKQGFHSGTAAASFLPSALGSGGPINPATAAAYPPAPFM 1032
733 HILPAHQPHSQLHHLHPQDAQ 755
1033 HILTPHQPHSQLHHLHQDQ 1055

RESULT 13
ID Q8K102 PRELIMINARY; PRT; 1105 AA.
AC Q8K102;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE NICE-4 protein homolog, isoform 1.
GN Name=4932431F02Rik;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=1105 AA; 116903 MW; 3DD82C85DE1B188A CRC64;
RA Strauberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029075; AAH29075.1; -;
DR MGI; MGI:1921633; 4932431F02Rik.
DR InterPro; IPR000449; UBA.
DR InterPro; IPR009060; UBA_like.
DR Pfam; PF00627; UBA; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00030; UBA; 1.
SQ SEQUENCE 1105 AA; 116903 MW; 3DD82C85DE1B188A CRC64;
Query Match 37.2%; Score 1507.5; DB 2; Length 1105;
Best Local Similarity 45.1%; Pred. No. 2.1e-54;
Matches 363; Conservative 109; Mismatches 207; Indels 125; Gaps 30;
Qy 3 PGTGSSTAVNSCPQSLSSVLSGSGFGLAPPKMANITSSQILDQLK-APSLGQFTTTPST 61
Db 347 PASGS-----TPSHHSMVSMGLKGFVGDEAKGSGTTSQFLQFKTAQALAA---- 397
Qy 62 QQNSTSHPTTTTWDKLPQTSQSSVLSHLDFKQPEPSPVLSQLSQRQ----- 109
Db 398 -QHSQSGSTTTSSWDM-GSTQSPSLVQYDLKSGAND-STVHSPFTKQAFTPSSMTMEVF 454
Qy 110 -QHSQAV-----TVPPGLESPSQAKLRESTDSPSTVKNLQLSTTIENISVHQ 164
Db 455 LQKPPAVATSTAAPPPSPPLPSKS---TSAPQMSGSSDNQSSP-----Q 499
Qy 165 PPKHKLAKRRIPPAKIPASAVEMPGSADISGLNLFQFGLQFSGSPVLSDYESTPTTS 223
Db 500 PAQKLLKQKKTSLSKIPALAVEMPGSADISGLNLFQFGLQFSGSPVLSDYESTPTTS 559
Qy 224 ENSNQIPISLYSKLSBLPLNTSLMTSAVQNSTYTTTSVITSSCSLTSSLSASPVAMSSS 283
Db 560 ASSSQAPSSLYTSTASESSSTVSNQS--QESGYQSGPIQSTTYTSQN-NAQGPL----- 611
Qy 284 YQSSVHNRIPIYQSPVSSSESAPGT-IMNGHGGGRSQOTLDTPTKTPG-----PSALPSV 337
Db 612 YEQRSTQTR-RYPSSISSSPQKDLTQAKNGFSSVQATQLOTTQSVGATGSAVKSESPT 670
Qy 338 SSILPS---TTSCCTALLPSTQ-----HTGDLTSSPLSQLSSLSHSSQSSLSAHAAL 385
Db 671 SSIPSLNETVPAASLLTANQHSSLSGLSHTBEIPNTTTTQHSSALSTQNTLSSTSS 730
Qy 386 SSSTSHT--HASVES--ASHQSSATFTSTAATSVSSSSAGSVLSSSMNTANSCLGCTPA 442
Db 731 GRTSTSTLLHTSVESSEANLHSSSTFTSTSTVSAPPVPV-VSVSSLSNCSGLSLGSGN 789
Qy 443 SASSSSRAPLVTSGKAPENLPQGVPPPLLNQVLPGLLPAYP--IYGYDELOMLQS 500
Db 790 STVTASTRSSVATTSGKAPENLPQGVPPPLLPNPYIMAP-GLLHAYPPQVGYDDQLQOT 848
Qy 501 RLPVDYVYGIFFAAPT-AASRDRLANNPVGDTKFGSDSASPAPATTPAQPOQSSQSO 559
Db 849 RFLDYYSIFPPTPTTLCRDCGLASNPVSGDLTKFGRGDSSAPATTLAQPOQNTQ 908
Qy 560 THHTAQOQFVNPAALPPGYSTGLPYTT---GMPSAFOYGTMPF-VPPASAKQHGVLNLS-- 613
Db 909 THHTTQOTFLNPAALPPGYSTGLPYTTGVCLPSTFYQVPAVPVAPTSKQHGVLNLSVN 968
Qy 614 TPTPPFOQAGYQGHGYSYTGVDLDTQGTAAAGDYSKGGYAGSSQAPNKSAGSGPKGVSVS 673
Db 969 ASATPPFOQPSGSGHGYNT-----GVSVT 992

181 PPSLSVLGSGTGLASGAAPGYAPPPFLHILPAHQPHSOLLHHLLPQDAQSGGSGRSQ 240
 QY 764 PSSLOPKSQASKPAYGNSPYWTN 786
 Db 241 PSSLOPKSQASKPAYGNSPYWTN 263

RESULT 15

AAH07890 PRELIMINARY; PRT; 263 AA.
 AC AAH07890;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DE UBAP2 protein (Fragment).
 GN UBAP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC007890; AAH07890.1; -.
 FT NON TER 1
 SQ SEQUENCE 263 AA; 27178 MW; 469D4F3ABEFDDE41 CRC64;

Query Match 35.3%; Score 1433; DB 2; Length 263;
 Best Local Similarity 100.0%; Pred. No. 5.6e-52;
 Matches 263; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 524 LANNYPGVDTKFGSDSASPAPATTPAQOQSQSTHTTAQPPFVNPALPPGYSYTGLP 583
 Db 1 LANNYPGVDTKFGSDSASPAPATTPAQOQSQSTHTTAQPPFVNPALPPGYSYTGLP 60
 QY 584 YTTGMPSAFYGTFTVPVPPASAKOHGVLNSTPTPPQOASGYGQHGYSYTGDDLTQGTAA 643
 Db 61 YTTGMPSAFYGTFTVPVPPASAKOHGVLNSTPTPPQOASGYGQHGYSYTGDDLTQGTAA 120
 QY 644 GDYSKGYAGSSQAPNKSAGSGPGKGVSVSSSTTGLPDMTGSVYNTQTDFKQGHAGTP 703
 Db 121 GDYSKGYAGSSQAPNKSAGSGPGKGVSVSSSTTGLPDMTGSVYNTQTDFKQGHAGTP 180
 QY 704 PPSLSVLGSGTGLASGAAPGYAPPPFLHILPAHQPHSOLLHHLLPQDAQSGGSGRSQ 763
 Db 181 PPSLSVLGSGTGLASGAAPGYAPPPFLHILPAHQPHSOLLHHLLPQDAQSGGSGRSQ 240

674 SSTTGLPDMTGSVYNTKTQTFKQGHAGTP-PPSLSVLGSGTGLASGAAPGYAPPPF 731
 Db 993 SSNTGVPDLSGSVYKTSQSFQKQGHAGTCTPAASFNLPSALGSGGFINPATAAAYPPAPF 1052
 QY 732 LHILPAHQPHSOLLHHLLPQDAQ 755
 Db 1053 MHILTPOQPHSQILHHLLQDQDQ 1076

RESULT 14

Q6PK34 PRELIMINARY; PRT; 263 AA.
 AC Q6PK34;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE UBAP2 protein (Fragment).
 GN UBAP2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
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 Db 121 GDYSKGYAGSSQAPNKSAGSGPGKGVSVSSSTTGLPDMTGSVYNTQTDFKQGHAGTP 180
 QY 704 PPSLSVLGSGTGLASGAAPGYAPPPFLHILPAHQPHSOLLHHLLPQDAQSGGSGRSQ 763

Qy 764 PSSLOPKSOASKPAYGNSPYWTN 786
Db 241 PSSLOPKSOASKPAYGNSPYWTN 263

Search completed: January 31, 2005, 17:47:01
Job time : 210 secs

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